0 / 197 ho

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GenCore version 5.1.3
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UM protein - protein search, using sw model

Pun on:

January 28, 2003, 11.43:11, Search time 39 Seconds (without alignments) 1387.173 Million cell updates/sec

US-09-828-432-3

QPNPPIPWEHEDQETGEGVK 1 MNVSFAHLHFAGGYLPSDSQ. Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 segs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

seg length: 0 seg length: 2000ουρορ Minimum DB Maximum DB

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

| SIDS2/gagdata/geneseq/geneseqp-embl/AA1990.DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		Description	Human HGPRBMY7 N-+	Himan HGPRRW77 C-F	Human G protein-co	Novel G-protein co	Galanin receptor=1	Human G-protein co	Amino acid semieno	Human G-protein co	Himan DNA G-protei	Human G protein-co
		σı	AAU98047	AAU98048	ABG61638	AAU10631	AAU08807	AAE06761	AAG63344	AAU04363	AAU01848	AAB60691
			23	23	60	23	22	C1	22	CI CI	22	22
		Watch Length DB	406	406	40E	406	419	419	419	419	419	419
ap.	Query	Match	100.0	100.0	100 D	100.0	100.0	100.0	100.0	100.0	100.0	1000
		Score	2167	2167	2167	2167	2167	2167	2167	2167	2167	2167
	Result	No.	1	2	3	4	2	9	7	89	6	10

27-SEP-2000; 2000US-235731P.

Novel Guratein co	Gprotei	9000	han G profe	uman rotential G	an 52874 G pr	Total Cour	n G protein	alanin re	e dalanin rec	> dalanin re	se dalanin	31.11.11	daiati.ti T	at dalanin r	at Gaine It	t Jakahil.	at dalanin recer	at galanin r	at galanin r	31 13 4111	at GalR2 rec	t qalanin	at qalanın r	at galanin 1	t galanin	qalanin	an qalan	qalanin r	dlan.	dalanın ı	an dalanin r	galahin 160	e pancreas b	s pancreas 3-
AAU1063	AAE170	AAG6334	AAG6412	AAU732	AAU9790	AAUSSES	ABG6164	AAW6146	AAW6133	9 AAW49004	AAU7454	AA74512	AAB6513	AAG6821	AAW4013	AAW2456	AAW6138	AAW4900	AAW6146	AAW5225	AAW4013	AAY4513	AAB6513	AAU7454	AAG6821		AAWS225	AAW2456	AAW6146	AAWG138	AAW4900	AAU7454	<b>AAR</b> 950	AAR9122
7	e,	9	6	18	61 2	37 2	10 2	71 1	71 1	371 19	71 2	16 2	46	46 2	72 1	72 1	72 1	72 1	72 1	72 1	72 1	72 2	7.2 2.	72 2	72 2	58 2	35 1	37 1	37 1	37 1	37 1	37 2	18 1	18
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$\vdash$	4	16	16	9	05	3	59	70.	7C.	270.5	70.	9	. 69	69.	ω	O.	S	S.	w	9	S	S	10	(a)	5.6	265.5	S	w	10	10	w	10	in	Lin.
11	13	13	14	15	16	17	18	19	20	21	CI CI	23	함	25	56	27	28	50	30	31	32	33	34	32	36	37	38	39	0.4	41	42	4ع	44	45

#### ALIGNMENTS

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faces "The Noterminus can be optionally and sequentially deleted by one amino acid at a time"
                                                                                                                                                    Human; G protein-coupled receptor; HGPRBMY7; spinal chord; spinal chord-related disorder; breast cancer; neoplastic disease; brain disorder; leukaemia; myeloma; immunological disorder; cholecystitis; drave's disease; osteoarthritis; asthma; neurological disorder; dementia; depression; Alzheimer's disease; Down's syndrome; epilepsy; intracellular calcium level; NPAT; nuclear factor activator of transcription element; mutant; mutein.
                                                                                                                       Human HGPRBMY7 N-terminal deletion mutant representative sequence
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                               AAU98047 standard; Protein; 406 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-2001; 2001WO-US30351.
                                                                                          13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                              Misc-difference 1..399
                                                                                                                                                                                                                                                                                                                                                                                                           WO200226823-A2
                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-2002
                                                                                                                                                                                                                                                                                                   Synthetic,
RESULT 1
AAU98047
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The invention relates to an isolated polypeptide (I) comprising amino acid sequence that is at least 95% identical to a polypeptide fragment of a fully defined human 9 protein-coupled receptor BMY2 (HSDRBMY2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide, or variant, alleft coupping the above bolypeptides.

Also included are polynuclectides encoding the above polypeptides, whereasten vertees, however, and its polynucleotides and modulators of HGPRBMY. And its polynucleotide are useful for diagnosis prevention, treating or ameliorating a medical condition e.g. a disease, disorder, or a condition related to brain, breast, gastrointestinal or energial systems, such that thalamus, corpus callosum, cerebellum, caudate nucleus, amygdala, substantia nigra, hippocampus, brain, breast, colon, spinal chord-related disorders, hippocampus, brain, breast, colon, spinal chord-related to spinal chord and brain. An antagonist or inhibitor of (1) identified using (1) is useful for treating a neoplastic disorder such as leukaemia, myeloma, immunological disorders such as eleukaemia, myeloma, immunological disorders such as leukaemia, myeloma, immunological disorders such as eleukaemia, myeloma, immunological disorders such as leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      days) human a protein coupled reserver PMT2 (Happamy2) polypeptide, useful for modulators of HGPRBMY2 activity that are useful for treating leukaemia, cholecystitis, Grave's disease, epilepsy, dementia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide are useful for modulating intracellular calcium levels, modulating Cafot sensitive signalling pathways and modulating nuclear fartor activator of transcription (NRFT) element associated signalling pathways. The present sequence is a representative sequence for a set of sequential Noterminal deletion mutants of HGPRRMY7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 VAREBEWSMERKLYRLLARGIDLEFASFYFWRAYDGGYWFGGYTGHLRNGIRSYGWTWWLL 240
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                                                                                                                                                                                                                                                                                                                              Feder JN, Mintier G, Ramanathan CS, Westphal R; name A, Barber L, Kornacker MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        osteoarthritis, asthma, neurological disorders such as dementia, depression, Alzheimer's diseaso, Down's syndrome and epilepsy. HGPRBMY7, its polynucleotide and agonists or antagonists of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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100.0%; Prod No. 2 5e 191;
ative 0; Mismatches 0;
                                                                                                                                                                                    (BRIM ) BRISTOL-MYERS SQUIBB CO
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14-FEB-2001; 2001US-268580P.
28 AMG 2001; 2001US-215423E.
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AST KTEYAEIPILPNVEQFWHEPDTVPSVQNNGPIPWEHENQETGEVV 406

Claim 12, Fig 2, 170pp, English.

depression

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/note= "The C-terminus can be optionally and sequentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human G-protein coupled receptor HMY7 (HGPFHMY7) pripperies, useful for modulative of HGFEHMY7 activity that are useful to the transfer enia, cholecystitis, Grave's disease, epilepsy, dementa.
                                                                                                                                                                                 Human; G protein-coupled receptor; HGPRPMV7; spiral objects, spinal chord-related disorder; breast cancer; need lastic licenses, brain disorder; leukaemia; myeloma; immunological disorder; cholecystitis; Grave's disease; osteoarthritic; action, netten; neutonogical disorder; dementia; depression; Alzhermor's disease; Down's syndrome; epilopsy; intracellular calcure level; NEFT; nuclear factor activator of transcription element; mutant; mutant; mutant.
                                                                                                                                                            Human HGPRBMY7 C-terminal deletion mutant representative sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feder JN, Mintier G, Ramanathan TT,
                                                                                                                                                                                                                                                                                                                                                                        deleted by one amino acid at a time"
361 KTEFABLILLEDVEQFWHERSTVFSVGNGDFTFWHHLDGLTOP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cacace A, Barber L, Kornacker MG;
                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                               AAU98048 standard; Protein; 406 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 FEB 2001; 2001US 268580P.
28-AUG-2001; 2001US-315423P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-2001; 2001WO-US30351.
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                                                                                                                                  13-A75-2077 (first entry)
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                                                                                                                                                                                                                                                                                               sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             04-APR-2002
                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                         AAUGRO48;
                                                                  AAU99048
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                   modulating Ca^2^+ sensitive signalling pathways and modulating nuclear factor activator of transcription (NFAT) element associated signalling pathways. The present sequence is a representative sequence for a set of sequential C-terminal deletion mutants of HGPRBMY7.
                                                                                                                                                                                                                                                                                                                                                                61 HCLILNLCLAFLSLLLFSAPIFATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                           180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 PEGLYGVWYWMITKKPPTVSFSQFTPAGNSEGLPDFVPSPESPASIPEKEKPSSPSGGG 360
                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                     1 MNVSFAHLHFAGGYLPSDSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGKPSMI 60
polypeptide are useful for modulating intracellular calcium levels,
                                                                                                                                                                                                                                                                                                                   1 MNVSFAHLHFAGGYLPSDSQDWRTIIPALLVAVGLVGFVGNLCVIGILLHNAWKGKPSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KVCFMYASDPAKQVSIHNYTIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 KYCFMYASDPAKQVSIHNYTIMSVLVAIMTVASLLPLPEWFFSTIRHHEGVEMCLVDVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 VAEEFMSMFGKLYPLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 SIAIISALLWLFEWVAWLWVWHLKAAGPAPPQGFIALSQVLMPSISSANPLIFLVMSEEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, G protein coupled receptor, HGFKBMY7, spinal chord, spinal chord-related disorder; breast cancer, neoplastic disease; brain disorder; leukaemia; mweloma; immunological disorder; cholecysticis; carav's disease, osteoarthribis; asthma; neurological disorder, dementia; depression; Alzheime; s disease,
                                                                                                                                                                                                                                                                                                                                                                                                         61 HSLILNLSLADLSLLLFSAPIRATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 VAEBFMSMFGKLYPLLAFGLPLFPASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLL
                                                                                                                                                                       Score 2167; DB 23; Length 406;
pred. No. 2.5e-191;
0; Mismatches 0; Indels 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Down's Syndrome; epilepsy; intracellular calcium level; NFAT;
nuclear factor activator of transcription element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 KTEKAEIPILPDVEQFWHERDTVPSVQDNDPIPWEHEDQETGEGVK 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTEKAEIPILPDVEQFWHERDTVPSVQDNDPIPWEHEDQETGEGVK 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human G protein coupled receptor MGPRBMY7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABGolésa standard; Protein, 406 AA.
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                                                                                                                                                                               100.0%;
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14-FEB-2001; 2001US-268580P.
28-AUG 2001; 2001US-315423P.
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                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 406; Conservative
                                                                                                                                   406 AA,
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                                                                                                                                        Sequence
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Polypeptide, or variant, allein variant or species homologue.
Also included are polymolectides encoding the above polypeptides, appression vertors, host cells, anti-HGPPBMY7 antibodies and modulators of HGPRBMY7. HGPRBMY7 and its polymolectide are useful for diagnosis prevention, treating or ameliorating a medical condition e.g. a disease, disorder, or a condition related to brain, breast, gastrointestinal or musculo-skeletal systems, such that thalamus., corpus callosum., caudate nucleus-, amygdala-, substantia nigra-, hippocampus-, krain-, heast-, colon-, spinal chord-related disorders, breast cancer, neoplastic diseases, and disorders related disorders, broad and brain An antagonist or inhibitor of (1) identified using (1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is useful for treating a neoplastic disorder such as leukaemia, myeloma, immunological disorders such as cholecystitis, Grave's disease, osteoarthritis, asthma, neurological disorders such as dementia, depression, Albeimer's disease, Down's syndrome and epilepsy. HGPRBMY7, its polynucleotide and agonists or antagonists of the polypeptide are useful for modulating intracellular ralcum ievels, modulating Ca<sup>2</sup>, sensitive signalling pathways and modulating nuclear factor activator of transcription (NRAT) element associated signalling pathways. The present sequence is the HGPRBMY7 protein sequence.
                                                                                                                                                                                                                                                    Novel human G protein coupled receptor EMY7 (HGPREMY7) polypoptide, useful for modulators of HGPREMY7 activity that are useful for treating leukacmia, cholecystitis, Grave's disease, epilepsy, dementia, depression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 KVCFMYASSPAKQVSIHNYTIMSVLVAIWTVASELPEPEPEPESTIRHHEGVEMCEVDVPA 180
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                                    Barber L, Kornacker MG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Fig 2; 170pp; English.
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Matches 406; Conservative (
    Feder JN,
                                         Cacace A,
                                                                                                                                 WPI; 2002-435195/46.
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                                                                                                                                                                               N-PSDB; ABK84809
    Battaglino P,
                                                  Hawken DR,
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RESULT 4

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compound modulating activity preferably neuropeptide binding or signalling of [11] and for purifying a 9 protein from a sample containing the G protein. The polynucleotide [1] is useful for identifying a compound which binds to [1] encoding [11] and for identifying an animal homologue of [11] The method comprises DNA hybridisation or computer homology searches to identify analyse and sequences of the animal that are homologous to [1]. The compounds identified by the screening methods
                                                                                                                                              d protein coupled receptor, 5PCP-2017, human; antiinflammatory; lamminosippressive, cerebropictative, tranquiliser, anticonvulsant montropic; neuroproteinive, human imminodeliciency virus; HIV, diaberes, cristati, montal disorder, thyroid disorder, across, cell differentiation; homeostasis; movement disorder, disorder, stroke; Huntington's dasease.

Tourette's Syndrome, dyskineda, attention disorder, movement disorder, parkinson's disease; Alzheimer's disease; ataxia; supranuclar palsy; metabolic disorder, cardiovascular disorder, annovement disorder, annovement disorder, perkinson's profilerative disease; periasis; hyperprofilerative disorder, hermonal disorder, perkinson's governant syndrome; alopecia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes the novel isolated G-protein coupled receptor protein-2017. The polypectide (II) is useful as a vaccine in a manual against (II); for identifying a compound binding to (II) proforably compounds useful for treating mental disorders; for identifying a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polymurlentide encoding novel G protein-coupled receptor-2037 and polypeptide useful for identifying modulators useful for treating disorders such as autoimmune disorders, stroke, diabetes, cancer,
                                                                                                                    Novel G-profein coupled receptor 2017 (nGPOP-2017) version #2
                                                                                                                                                                                                                                                                                                                                                                                                                     28..50
/label- Transmembrane_domain_1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane domain 5
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                                                                                                                                                                                                                                                                                                                                                                                                   location/Qualifiers
              AAU10631 standard; Protein; 406 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 31; Page 61; lolpp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PHAA ) PHARMACIA & UPJOHN CO
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05-DEC-2000; 2000US-251313P.
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                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    aloperia, anorexia
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                                                                                                                                                                                                                                                                                                                                                                  Home sapiens
                                                                                    05-JUN-2002
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                                               AAMIO631;
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AAU10631
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failure, inflammatory conditions of Crohn's disease, diseases related to cell differentiation and homeostasis, theusated antitities and cummunicated management diseases. Our diseases of cross of the such as Huntington's disease or Tourette's Syndrome, it entits in listadors, and degenerative diseases are partially as Parkinson's, Alizheument is, movement diseases, including ataxias, supranuclear palsy, industrials, such as viral infertions caused by human immunodeficiency rither (HIV) for HIV).
                                                                                                                                                                                                                                                                                                     metabolic and cardiovascular dispasos and dispudóns o q. 19p. 1 diaboton, anorexia, proliferative diseases and cancers, and hyperproliferative
are useful for treating disorders which include thyourd discultus, remai
                                                                                                                                                                                                                                                                                                                                                                                disorders such as psortasis, hormonal disorders collyclycycle continual syndrome, alopecia, among others. This is the amine and september to the linear novel G gattein coupled receptors for content of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dalamin receptor-like G protein coupled receptor, anoroctic; antidiabetic; cardiovascular; antiasthmatic; unchesic; on objectsont; vasorpric; pourotropic; antimigramo; transpilitation; dynamo; periorical; agree therapy; perhybysiological disculation; periorical; energy proceeding periorical; energy proceeding for the periorical describes the period of the period of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 2167; DB 23; Lemeth 407; 100.0%; Pred. No. 2.5e-191; tive 0; Mismatches 0; Indeis 7;
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W-200168843-A1.

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galanin receptor-like G-protein coupled receptor for therapeutic purposes, useful for treating disease by gene therapy. A pharmaceutical composition described in the specification is useful for modulating the activity of the Galanin receptor-like GPCR in a pathophysiological disorder, selected from obesity, diabetes, cardiovascular disease, asthma, pain, depression, ischaemia, Alzheimer's disease, sleep disorder migraine, anxiety and reproductive disorder. Specifically, the composition is useful for modulating the activity of the receptor in cognition, analgesia, sensory processing, processing or visceral information, motor coordination, modulation of dopaminergic activity and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VAEEFMSMFGKTYPLPAFGLPLPFASPYFWPAYPQCFKFGTKTQNLRNGIRSKQVTVMLL 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       314 PEGLIKGVWKWMITKKPPTVSESQETPAGNSEGLPDKVPSPESPASIPEKEKPSSPSSGKG 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                            Reagent and methods of regulating a galanin receptor-like G protein coupled receptors and their regulation for therapeutic purposes e.g. treatment of hypotension and asthma -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuroendocrine function. This sequence is the Galanin receptor-like 
G protein coupled receptor described in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes novel reagents and methods of regulating a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 MNVSFAHLHFAGGYLPEDSQDWFTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGKPSMI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 0%; Score 2167; DB 22; Length 419;
100 0%; Pred No. 2 6e-191;
ive 0; Mismatches 0; Indels 0;
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                                             16-MAP-2000; 2000US-0189898
                                                                1860100-810000
                                                                                        07-DEC-2000; 2000US-0251515
15-MAP 2001; 2001WG-EP02929
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Best Local Similarity
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361 KTEKAEIPILPDVEQFWHERDTVPSVQDNDPIPWEHEDQETGEGVK 406
                                                 374 KTEKARIPILPDVEQFWHERDTVPSVQDNDPIPWEHEDQETGEGVK 419
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Human; G-protein coupled receptor-11; GCREC-11; cytostatic; hepatotropic; virucide; antinflammatory; anticonvulsant; antiemedic; neuroprotective; nootropic; cerebroprotective; hypotensive; tranquilliser; vulnerary; ophthalmological; cell proliferative disorder; actinic keratosis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; anorectic; arteriosclerosis; atherosclerosis; cirrhosis; hepatitis; huntington's disease; Parkinson's disorder; stroke; Altheror'e disorder; epilepsy; hypertension; varioose vein; vasculitis; dysphadia; dyspepsia) anorexia; gastrointestinal disorder; panoreatitis; autoimmune disorder; Addisor's disease; Crohn's disease; acquired immune disorder; AlDS; uvetis; infection; transgenic animal; gene therapy.
                                                                                                               Human G-protein coupled receptor-11 (GCREC-11) protein.
16-OCT-2001 (first entry)
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Homo sapiens.

/label= 7\_transmembrane\_receptor\_domain /label= 7\_transmembrane\_receptor\_domain 41..61 /label= Transmembrane\_domain Location/Qualifiers Yue H, 02.FEB.2000; 2000US-0180093. (INCY-) INCYTE GENOMICS INC. 01-FEB-2001; 2001WO-US03455 Au Young J, WO200157085-A2 09-AUG-2001 Domain Domain Domain

WPI; 2001-488869/53. N-PSDB; AAD12954. Baughn MR,

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Novel isolated human G-protein coupled receptor useful for diagnosing, preventing and treating cell proliferative, neurological, cardiovascular, gastrointestinal, autoimmune/inflammatory and metabolic

Claim 1; Page 119-120; 138pp; English.

The present sequence is human G-protein ccupled receptor-11 (3CREC-11 protein. The present invention relates to GCREC protein and nucleic acids encoding them. 3CREC protein, its against or animatonic are useful of the conditions associated with dereseed expression or overexpression of functional GCREC in a patient, where the disorder is selected from cell proliferative disorders such as actinic bearings. Carteriosclerosis, atherosclerosis, cirrhosis, hepatitis, psoriasis, and cancer, neurological disorders such as epilepsy, stroke, Alzhenmer's disoase, Huntington's disease, Parkinson's disease, cardiovascular disorders such as dyspettain, and and action and adjoint and as diabetes. Chair circuit, viral, bacterial, lungal, parasitic, protections, trauma and metabolic disorders such as diabetes, obserty, osteoporogis. GFREC proteins and their cDNAs are used to assess the effects of exogenous compounds on the expression of GCREC sequences. GCREC cDNA is useful to create knock in humanised animals (pigs) or therapeutic or diagnostic purposes, for somatic or germline genetherapy, to generate hybridisation probes useful in mapping the naturally occurring genemic sequence, and in molecular biological transgenic animals (mice or rats) to model human disease, for

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23-DEC-1999;
23-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 SIAIISALLWIPEWVAWLWVWHLKAAGPAPPQGFIALSQVLWFSISSAUFIIFLVMSEEF 312
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                                                                                                                                                                                                                   1. MONOSFABLHENDANTECCOCEMETER ALL VAVILATEVECENTERLAMPEREMT 69
14. MONOSFABLHENDAGOVEDEDOÇDMETERALVAVOLVSEVƏRICVETLIBARMAMPGREMT 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amino acid sequence of a human G-protein coupled receptor protein.
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                                                                                                            100.0%; Score 2167; DB 22; Length 419;
100.0%; Fred. No. 2.6e 191;
ive 0, Mismatches 0, Indels 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT KIEKARIDILDPVEÇEWHERDIVESVƏRNEPIEWFHERQETSEGVE 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             374 KIEKAEIPILPIVEOFWHERDIVPSVGUNIFIFWHERGEFSFSVK 419
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                                                                                                                                                                                                                                                                                                                                                                                                        Endogenous and non-endogenous versions of human G-protein coupled receptors for direct identification of candidate compounds as agonists,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 SIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VAEEFMSMFGKLYPLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLL 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 VAEBFMSMFGYLYPLLAFGLPLFFASFYFWPAYDQCKKPGTKTQNLRNQIRSKQVTVMLL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 SIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEF 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                          inverse agonists or partial agonists for use as therapeutic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2167; DB 22; Length 419; 100.0%; Pred. No. 2.6e-191; tive 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 91-92; 160pp; English.
                                                                                                                                                                                                                                                                                                                            Dang HT, Lowitz KP;
                                                                                                        2000US-0196078.
                                                                                                                                                                                           200005-0226760.
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                                                          200011S-0189259.
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          99US-0171902
                                        2000US-0189258.
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26 SEP-3
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reproduction and sexual medicine, inflammation, cancer, tissue repair, dermatology, skin pigmentation, photoaging, frailty, osteoporosis, cardiovascular disease, gastrointestinal disease, antiinfection, allergy and respiratory disease, sensory organ disorders, sleep disorders
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Antibodies against PPI-001 and compounds which modulate its activity are useful as pharmaceuticals, for manufacturing a medicament for treating a patient having a need to modulate (i.e. (selectively) antagonise or agonise) PFI-001, and for evaluating and/or screening agents that can modulate PFI-001. The nucletc acid is also useful in gene therapy. The nuclet caid and encoded protein are useful for screening drug candidates for treating diseases associated with signal transduction such as obesity, diabetes and metabolic disease, neurodocical disease, psychotherapeutics, urogenital disease,
                                                                                                                                                                                                                                                                                                                        chromosome 5; antibody; immunogen; signal transduction; obesity; diabetes, metabolic disease; neurological disease; psychotherapeuiles; urogenital disease; reproduction; sexual medicine; inflammation; cancer; tissue repair; dermatology; skin pigmentation; photoaging; frailty; osteoporosis; cardiovasculat disease; gastrointestinal disease, antiinfection, allergy; respiratory disease; sensory organ disorder; sleep disorder; hair loss; mutein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptide, useful in drug screening, as well as diagnosing of treating diseases associated with signal transduction, e.g. obesity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence represents PFI-001, a Human G protein coupled receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New human G-protein coupled receptor (GPCR) polynucleotide and
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                                                                                                                                                                                                                                                                                                Human; G-protein coupled receptor; PFI-001; mutant;
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o
                                                                                                                                                                                                                     Human DNA G-protein coupled receptor, PFI-001.
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100.0%; Pred ...
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AAU01848 standard; Protein; 419 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-2000; 2000EP-0308851.
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                                                                                                                                                  07-SEP-2001 (first entry)
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AXCR40; Luman, G protein-compled receptor, 7TM receptor, fall2 galamin receptor homologue; chromosome 5q31-32; infection, viral; bacterial; bingal; proteozon, HIV-1; infection, viral; bacterial; bingal; proteozon, HIV-1; path, cacter, distance, distance, distance, distance, distance, distance, hyportension; angina partoris; every caste heart failure; hyportension; hyportension; hyportension; hyportension; angina partoris; propertial included in a received distance, and distance distance, depression; distance demonstrate retardation, dyskinesia, Parkinson's disease; Bintingian's disease; drug screening; signal transduction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74 HSLIDMLSLADLSLLEFSADIBATAVSESWWDLGWFVCKSSDWFIHFGMAAKSLTIVVVA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATISALLWIFEWVAWIWVWHLKAAGFAPPQGFIALSQVLMFSISSANFLIFLVMSEEF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          254 SIALISALLWIPEWYAWIWWHIKAAGPAPPQGFIALSQVIMFSISSANPLIFLVMSEEF 313
61 HSLILNLSLADLSLLLFSAPIRATAYSKSVWDLGWFVCFSSDWFIHTGMAAKSLTIVVVA 120
                                                                                                                                                  134 KUCEMYASDPAKQUSIHNYTIWCULVAIWTVASLLPLPEWFFSTIPHHEGVEMCLVPVPA 193
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                                                                                                                                                                                                                                                                                                        VARREMSMEGKLYELJAFGLEJEPASFYEMBATIZ (1478.37F), 1419.00 SF ZVTVMJ.
                                                                                                                                                                                                                                                                                                                                                                                     194 VABBEMSMESKLYFLLAFSLETFFASEVEWFARTSCFFFSSTFTSHEDDIFFFSFYDVTVMLL
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N FSDB; AAF59994.
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AAR60691
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The invention relates to the human giptotein compact theory: AX be standards. Like all Giptotein-compled receptors, AX be standards. Common and variants. Like all Giptotein-compled receptors, AX be standards. Discated and variants and structural similarity with Giptotein complete the AX be be compacted and structural similarity with Giptotein complete the formal cases of the man and marginal receptor. The human AX be contained to a theory and structural similarity with Giptotein complete the cases of Still 12. The invention like relative to the cases of Still 12. The invention like relative to the case of Still 12. The invention like relative to the case of the many better including bacterial, fungal protected and AX order to the case of th
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Similarity 100.0%; Pred. No. 2.68 191;
Rf. Compoyyative 0; Mismatches 0; Indelts ;
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RESULT 11 AAU10630 σ

AAU10630 standard; Protein; 419 AA.

AAU10630;

(first entry) 05-JUN-2002 Novel G-protein coupled receptor 2037 (nGPCR-2037) version #1.

G-protein coupled receptor, GPCR-2037, human; antinflammatory; immunosuppressive, cerebroprotective, tranquiliser, anticonvulsant; nootropic, neuroprotective, human immunodeficiency virus; HIV; diabetes, cytostatic, mental disorder, thyroid disorder; renal failure; Crohn's disease; cell differentiation; homeostasis; movement disorder, ox disorder, stroke; Huntington's disease; Tourette's Syndrome; dyskinesis, attention disorder; movement disorder; degenerative disorder; Parkinson's disease; Alzheimer's disease; ataxia; aupranuclear palsy; metabolic disorder; cardiovascular disorder; anorexia; proliferative disease; psoriasis; hyperproliferative disorder; hormonal disorder; polycystic ovarian syndrome; alopecia.

Homo sapiens.

41..63 /label= Transmembrane\_domain\_1 76..98 /label= Transmembrane\_domain\_2 Transmembrane\_domain\_5 'label= Transmembrane\_domain\_b /label= Transmembrane domain 7 Transmembrane domain 3 Transmembrane domain 4 Location/Qualifiers 205..223 /label= Ti 170 252..274 .307 117..139 label= label= Domain Domain Domain Domain Domain Domain Domain 

WO200177175-A2.

18-0CT-2001

U6-APR-2001; 2001WC-US11331.

06 APP 2000, 2000US 195228P.

(PHAA ) PHARMACIA & UPJOHN CO

Seilitz T, Berthold M; Vogeli G, Lind P,

WPI; 2002:017449/02.

N-PSDB; AAS16253.

Polynucleotide encoding novel G protein-coupled receptor-2037 and polypeptide useful for identifying modulators useful for treating disorders such as autoimmune disorders, stroke, diabetes, cancer, alopecia, anorexia

Claim 31; Page 61; 101pp; English.

protein-2037. The polypeptide (II) is useful: as a vaccine in a mammal against (II); for identifying a compound binding to (II) preferably compounds useful for treating mental disorders; for identifying a compound modulating activity preferably neuropeptide binding or signalling of (II) and for purifying a G protein from a sample containing the G protein. The polynucleotide (I) is useful for identifying a compound which binds to (I) encoding (II) and for identifying an animal homologue of (II). The method comprises DNA hybridisation or computer homology searches to identify mucleic acid sequences of the animal that are homologous to (I). The compounds identified by the screening methods are useful for treating disorders which include thyroid disorders, renal The invention describes the novel isolated G-protein coupled receptor

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             to cell differentiation and homeostasis, rheumatoid arthritis, autoimmune disorders, movement disorders, CNS disorders e.g. stroke, dyskinesias and as mutingfood's disease or Tourette's Syndrome, attention disorders, and degenerative disorders such as Parkinson's, Alzheimer's, movement disorders, including ataxias, suprannucloar palsy, infections, such as viral infections caused by human immunodeficiency virus (HIV): 1 or HIV-2, metabolic and cardiovascular diseases and disorders e.g. type 2 diabetes, anorexia, proliferative diseases and cancers, and hyperproliferative diseases and cancers, and hyperproliferative diseases, hormonal disorders e.g. type 2 diabetes, syndrome, aloperia, among others This is the amino acid sequence of the human novel G-protein coupled receptor 2037 version #1 described in the
failure, inflammatory conditions e.g. Crohn's disease, diseases related
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                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 2167; DB 23; Length 419; 100.0%; Pred. No. 2.6e-191; tive 0; Mismatches 0; Indels 0;
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AAE17082 standard; Protein; 419 AA (first entry) 18-APR-2002 AAE17082; RESULT 12 AAE17082 

Human G-protein coupled receptor (GPCRx20) protein.

Human, G-protein coupled receptor; GPCPx20, rerehreprotective, vomiting; receptor-mediated disorder; thorapy; urinary retention; allergy; observed osteoporosis; anglain pectoris; restencis; allergy; observed; whychersion anorexia; tumour, migraine; acute heart failure; ulcer; antinflammatory; stroke, hypertension; neuronal disorder; mycatalal infarting; psychoric; depression; mental retardation, neurodegenerative disease; antibacterial Alzheimer's disease; dementia; isohaemia; Parkinson's disease; antiviral; Huntington's disease; anxiety, antifungal, immunosuppressive; cynorianio, vulnerary; analgosic; anorecties; cancer; tranquillizer; neuroleptic, antiemetic; vasotropic; diabetes; cancer; tranquillizer; neuroleptic.

Homo sapiens.

Key

Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New G protein coupled receptor, useful in the manufacture of medicaments for treating receptor mediated disorders orgularite bourt failure and Alzheimer's disease -
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                           "Tranimembrane dunain"
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11-JUL 26v0; 2000US-217494P.
26-JAN-2001; 2001EP-0870015.
12-FEB-2001; 2001EF 0870015.
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The present sequence represents a human G protein by the forming the season in the form large of the forming the season in the form the diseases including Mypertension, autoimmune diseases, breat the formation, autoimmune diseases, from the formation, autoimmune diseases, from the formation of the season formation of the format
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Human; G protein-coupled receptor, GPCR; GAL4, galamin receptor; Alzheimers's disease; amyorrophic lateral sclerosis; asthma; atheresclerosis, basal cell carsinoma, breast catching, callinguabily; chondrosarcoma; chronic obstructive pulmonary disease; CLOSH; v disease; chondrosarcoma; chronic obstructive pulmonary disease; CLOSH; v disease; multiple sclerosis; narolar degeneration; lymphoma; melanoma; multiple sclerosis; narolar degeneration; lymphoma; melanoma; psoriasis; rheumatoid arthritis; schizophrenia; ulcerative collitis; tuberculosis; cognition disorder; memory disorder; anorexia; hormonal release disorder; cardiovascular activity disorder; pain perception disorder; cardiovascular activity disorder; diabetes; obssity; diabetes; obssity; diabetes; obssity; diabetes; byschipidaemia; stroke; gene therapy.
     The invention relates to nine human guanosine triphosphate binding protein (5 profein) coupled receptors designated GPPv8, 5FRV12, GPRV12, GPRV14, GPRV47, GPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAEEPMSMESELVELLAPGLPLEFASPYFWEAVEGOPPESTRICHLENGISCLEGATAMIL 040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 HSEILNUSLADESELLFSAPIPATAYSKSVWDLGWFVCKSSPWFIHTCMAARSELTIVVVV 133
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                                                                                                                                                                                                                                                                                                                       99.9%, Score 2164, DB 22, 99.8%; Pred. No. 4.8e-191; attive 1; Mismatches 0;
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Matches 405; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; guanosine triphosphate binding protein-coupled receptor; of protein.coupled receptor; GPRV4; GPRV4; GPRV4; GPRV4; GPRV4; GPRV4; GPRV4; GPRV4; GPRV4; Alzheimer's disease; cytostatic; hepatotropic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194 VAEEFMSMFGKLYPLLAFGLPFFASFYFWPAYDQCKKRSJKTQNLPNQIRSKQVTVMLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                  181 VAFEPMSMFORI YPILLAFGLPLPPASPYPWPAYDQOKKPGTPTQNLFNQIRSYQVTVMLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254 SIAIISAVLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEF
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        Pred No 4.8e-191;
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99 A%; Pred w
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Matches 405; Conservative
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Novel G protein-coupled receptor polypeptides including galanin receptor polypeptides useful for identifying modulators that are useful for treating Alzheimer's disease, psoriasis, melanoma, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease. Preferably, compounds that decrease or increase the expression of galanin receptor (GAL4) can be used to treat obesity, diabets, hyperlipidaemia and stroke. The GPCR nucleic acid is useful for treating the above mentioned disorders by gene therapy techniques. The present sequence is a novel GPCR of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNVSFAHLHFAGGYLFSFSQDWRTIIPALLVAVCLVGFVGNLCVIGILLHNAWKGKFSMI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.8%; Score 2162, DB 23, Length 418, 100 0%; Pred. No. 7 44-191; tive 0; Mismatches 0; Indels 0
                                                                            Fabre-Suver C, Pritchard
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                                                                                                                                                                                                              Disclosure, Paye 122, 144pp, English.
                                                (LIFE-) LIFESPAN BIGSCIFNCES INC
                                                                            Miller M, Burmer G,
           11-MAY-2000; 2000US-203217P.
18-MAY-2000; 2000US-205945P
                                                                                                                   N-PSPR; AASGROAR, AASGRIGG
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                                                                                                      2002-066595/09
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                                                                                                                                                                                     sclerosis, stroke
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                                                                          Brown JP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated polypeptide encoded by a nucleic acid molecule that is at least 80% identical to the G nucleic acid molecule that is at least 80% identical to the G professor coupled (GPCR) polynucleotides included in the specification. Also included are probes based on the GPCP sequences (including antisense probes), a host cell comprising an expression vector comprising the GPCP sequence, antibodies raised against the polypeptides, and methods of identifying modulators of the polypeptides. The polypeptides are useful for identifying modulator compounds which function as modulators, activators, repressors, agonists or antagonists of the novel GPCP polypeptides including the GAL4 polypeptide. The antibodies and nucleic acid probes as described above can be used to deserve the presence of the polypeptides and nucleic acid probes as described above can be used to deserve the presence of the polypeptides in which GPCPs are involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cognition and memory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        depression, politics, marular degeneration, lymphoma, melanoma, multiple sclerosis, osteoarthritis, osteoporosis, Parkinson's disease, psoriasis, rheumatoid arthritis, schizophrenia, ulcerative colitis, tuberculosis and many other diseases listed in the specification. The probes and antibodies are also useful for diagnosing cognition and memory disorders, anorexia, hormonal release disorders, cardiovascular activity disorders, pain perception disorders, obesity, diabetes, Alzheimer's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           e.g., Alzheimer's disease, amyotrophic lateral sclerosis, asthma, atherosclerosis, basal cell carcinoma, breast carcinoma, cardiomyopathy, chondrosarcoma, chronic obstructive pulmonary disease, crohn's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 KUCEMYASIPAAKOVSTHNYTIWSVLVAIWTVASLLPLPEDPEWFFSTIRHHEGVEMCLVDVPA 180
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January 28, 2003, 11:48:36; Scarch time 35 Seconds (without alignments) 2390.147 Million cell updates/sec
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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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2: Sp. bacteria: *
3: Sp. Lung: *
4: Sp. human: *
5: Sp. invertebrate: *
6: Sp. ammal: *
7: Sp. mhc: *
10: Sp. phage: *
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11: Sp. rodent: *
11: Sp. vertebrate: *
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2167
1 MRVJPAHLHFAGGYLPSDSC
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Maximum DB seq length: 2000000000
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Perfect score.
Sequence.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

	Description	Q8tdv0 homo sapien		Q9nfv2 lymnaea sta	Q23497 caenorhabdi	Q9nfv0 lymnaea sta	Q9w6i3 gallus gall	Q925r4 cavia purce	Q9jkn0 mus musculu	Q8vhd7 rattus norv	Q9nfv3 lymnaea sta	Q9vau0 drosophila	Q9nbc8 drosophila	Q8qgm3 gallus gall	Q8wpa2 hombyx mori	Q9jk40 mus musculu	Q9ude6 homo sapien
SUMMAKIES	ID	QRIDVÔ	Q9NFV1	CONFUE	Q23497	OSNEVO	Q9W6I3	Q325R4	ONXL60	72HV8C	Q9NFV3	O9VAU0	Q9NBC8	QBQGM3	Q8WPA2	Q9JK40	្នាញាទទ
	DB	4	S	ωì	Ŋ	ហ	13	-7	11	7.7	S	Ŋ	S	13	(J)	11	4
	* Query Match Length	419	380	383	444	380	411	7	452	CCF	380	329	357	377	361	385	80.5
	% Query Match	100.0	11.6	•r ;;	10.9	10.7	10.6	10.6	10.5	10.5	10.2	10.1	10.1	10.0	σ: σ:	σ.	σ.
	Score	2167	251	247 5	236	232.5	230 5	230	228	C4 C4	220.5	218	218	217.5	214.5	214.5	214.5
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# ALIGNMENTS

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Saunders S.E., Burke J.F., Benjamin P.P., Control of a family of multimers of Earling sites in the promoter regions of a family of T.P. of professional sites in the promoter regions of a family of and nociceptin/orphanin-FQ receptor families "; Submitted (orr.1994) for the FMMI/GenBank/Orth/databases.

- SUBMILLAPITY RELOASTON FAMILY 1 OF G-PROTEIN (BY SIMILAPITY).

- SIMILAPITY RELOASTO FAMILY 1 OF G-PROTEIN GODIED PROFEPTORS.

- MILLAPITY RELOADS TO FAMILY 1 OF G-PROTEIN GODIED PROFEPTORS.
181 VAEEFMSMFGKLYPLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLPNQIRSKQVTVMLL 240
                          194 VAEEENSMESELXPILAPSLEPERSEYFWPAYPQCFFFFTQNLFNQIPSFQYTWNLL 553
                                                                                                                                                               241 SIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEF 300
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                                                                                                                                                                                                                                                                                                                                                                                                                   314 PEGLIKGVWWWMITFKPPTVSBSGETPAGNSBGLPPKVPSPRSPASIPEKEKPSSPSSGKG 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 Addianahiinpipspsysttiypphttaarinesmmpeeryelivptifsylcilgip 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Metazoa, Mollusoa, Gastropoda, Pulmonata, Basommatophora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 GNLCVIGILLANAWKGKPSMIHSLILNLSLADLSLLLFSAPIPATAYSKSVWDLGWFVCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 ILLOFGVENYVHEGENPSAČLNIKELKEPEAGKAFFGSFLFFGYVIPLGVIMLMYGLMLX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSTEP, PAGG237, G PPOTEIN_PEGEP_FL1; 1
PROSTEP, PSGG262, G_PPOTEIN_BEGEP_FL2; 1
G-protein; PSGG262, G_PPOTEIN_BEGEP_FL2; 1
G-protein; PSGG262, G_PPOTEIN_BEGEP_FL2; 1
SECURITE AND A FAMILY MW, ANDZAPPGGASUCAPA OPICK4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 11.6%; Score 251; DB 5; Length 380; Best Local Similarity 23.2%; Fred. No. 4.2e 12; Matches 89; Conservative 68; Mismatches 153; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               374 KTEKAFIPII PINUEQPWIEPITVPSVQPNDPIPWEHERGET3F3VK 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34: MTEMAFIPILPDVEQPWHERPTVPSVQDNDPIPWEHEPQETGEGVM 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9NFV1;
01-00T 2000 (TrEMBLrel. 15, Created)
01-00T-2000 (TrEMBLrel. 15, Last sequence update)
01-00T-2000 (TrEMBLrel. 11, Last annotation update)
G-profein coupled receptor
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Pfam, PP00001, 7tm_1, 1.
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PPINTS; PRO1570; NPFPRECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lymnaeidae, Lymnaea
NCBL TaxID-6523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; Pn2699; 1FAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O9NFV1
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293 HAPNTIFHISTMEAAACLAYMNGCVAPILLYAFLGENFERGFREEDS TOSTESSEWRFYSST 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 WEALLINTILLOGNIPILLOFSVENYVHEGENESAGLNIRETERFERGARAFEGETT...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 C. TIMPHING FOR CONTRACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 VIVVVIFAICWLFIQIILFABRFGHAPNTIFHISTMSAANCI,AYMNSCVNFILYAFILSEN 🚓
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46 RIIVPTIFGVICTLGLFGNSLVIPVVVSD - KHMRNTTNILLESGAVAGGEFFLFFTVEFFF (03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.1 1.47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sukaryota, Metazoa, Mollusha, Gastropoda, Pulmonata, Hassematribera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23 FILLPALLVAVÇIVGEVÇILÇERLEHMAMPOPPOMINCE ELMEGELE BEKENDE BE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 ATAYSKSVWDLOMPV/KESTWETHTOMAROUTTVVVARVOTEMYASIDARUUTTRV TTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DAO LOIAITSALLA PERCARIAGNING PAA UPA FUNETAL DITTAGO DE AGOTO DE SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITÉ, PSOAZAT, G PROTEIN PECEE EL L.
PROSITE, PSSAAZ, G PROTEIN RECEP EL Z.
G-PROTEIN COMPANIAN RECEP EL Z.
SEQUENCE - XEL AA, 41540 MM (17) FEMINANTE CROCK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%; Score 247.5; DB 5; Length **C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 PPEGEKGUW---------KWMITERPPTVSESÖBIPA 3NSE (4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              329 PRESPRINTICATESSERMEYERTWIPF PATETITE PATETION WAS 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68; Mismatches 144; Indels
264 KAAGPAPPQGFIALSQVLMFSISSANPLIFIJVMSEEFREGIJKGVW
                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Last sequence update of 01-JUN-2002 (TrEMBLrel. 21, Last annotation update
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 7,9e 12;
                                                                                                                                                                                                                                                                                                   380 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 WSVIVAIWTVA- -SILFLFFWFFSTTFHHFFTFMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 KLYFL---LAFSLFLFFACFYFWRAYDQCPFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymnaca stagnalis (Great pond snail).
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Pfam; PF00001; 7tm 1; 1.
                                                                                                       312 ----ITKKPPTVSESQETPAGNSE 331
                                                                                                                                                              353 VRFTVTEK-PTTTTTKOTCVNNSK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS, PRODZ37, GEGRRHODOPSN. PRINTS, PROIS70, NPFFREGEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                             G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 22.7%, ses 79, Conservative
                                                                                                                                                                                                                                                                                                     PPELINIMAPY;
                                                                                                                                                                                                                                                                                                                                                         -Cult-2000 (Tremplire)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lymnaeidae, Lymnaea.
NOBL_TaxID=6523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>úuery Match</u>
                                                                                                                                                                                                                                                                                                                               O9NFV2:
                                                                                                                                                                                                                                                                                                   COMMOD
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162 ALCFIVITITASQIPVG-----PMHCIYVYDFIMBKRSTČAILTIATABATPTMARTY 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 FM. SMFGKLYPLLAFGLPLFFASFYFWPAYDQCFKPGTKT---QNLRNQ----IR--- 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         232 ----SKQVTVMLLSIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFI------ 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85 AYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSI---HNYTI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 DYAAPTWIEPEWICSMINFFOHTSAYCSVWTLTI.MALDRYI.AVVYPVESMTLRTPRNTVI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 WSVLVAIWTVASLLPLPEWFFSTIRHH-----EGVEMCLVDVPAVAEE----- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GIBVVLTGIMERYIWPMPRPGMSQSVGGRWITMPDSGSSTPRP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 EATAAKREVTRIVICVLIIWALCWLPINVCRF ----MSGLAYPEPLVISHGVIMVIVQ 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 236; DB 5; Length 444;
; Pred. No. 7.9e-11;
60; Mismatches 127; Indels 68; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 IIPTIFAVIILVGLVGNALVVIVAFGROMR----NSTNTLIIGLAISDLMFLLLCVPFTAV 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lymnaea stagnalis (Great pond snail).
Eukaryota, Metazoa, Mollusca, Gastropoda, Pulmonata, Bascmmatophora,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 IIPALLVAVOLVGFVGNICVIGILLHNAWKGKPSMIHSLIINLSLADI,SLLLFSAPIRAT 84
                                                                                                                                                               Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology.";
Schone 28.12.02.2018 (1988).
SUPPELLULAP LICATION: INTESPAL MEMBRANE FFOTEIN (BY SIMILARITY)
-: SIMILARITY. BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFASTER PROMOTO, 7tm 1, 1. PROSEP F1.1, 1.
PROSTER: PROMOTO: G PROTEIN RECEP F1.2: 1
G-profein coupled receptor; Glycoprofein; Transmembrane.
SEQUENCE 444 AA, 49814 MW, 2CF41F429B302AE2 CRC64;
                                                                                                                                                                                                                                                                              Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                   01-NOV-1996 (TrEMBLrel 01, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     276 ALSQVLMFSISSANPLIFLVMSEEFREGLKGVWKWMITK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326 IASQVLAYTHSCLNPILYALMSQSPREGFIRVMFMLINK 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          380 AA.
                444 AA.
                                                                                                                                                                                        Phabditidae; Peloderinae; Caenorhabditis.
                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, 266567, CAA91489.1, -.
InterPro, IPPnnn276, GPCP_Phodpsn
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.3%,
24.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 24.8 es 84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                PRELIMINARY;
                                                                                                                                               Caenorhabdítis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 FMTFHVF3T/LPL
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=6239;
                                                                                                              Zr455 3 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                  023497;
                                                                                                                                 ZK455.3
                  023497
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023497
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 VVIVVVIFALCWEPIQILLEPAEREGHAPNTIEHISTMEAANCLAYMAGCTHELLYAFLSR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 RIIVPTIFGVICILGLFGNSLVILVVVSD--KHMRNTTNILILSLAVADLLFILFCVPFT 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 WSVLVAIWTVA----SLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEE-----FMS- MF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 GKLYPL----LAFGLPLFFASFYFWRAYDQCKKR. -----JTFTQMLENGIFSKGVTVM 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  223 GYVIPLGVTMLMYGLML------- KPLLYGVVFGGGNGSAESIRAFFRATRN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      239 LLSIALISALLWIPEWVAWLWVWHIKAAGPAPPOGFIALSOVLMFSISSANFLIFLV73E 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 ATAYSKSVWOLGWEVCKSSDWFIHTCMAAKSLTIVVVAEVCENYASLFAKGVSTRN-YT1 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104 ATGYALPVWPFGDIGCKMTQYAMYVCAYASVYTLVIMSLDRYLAVVHAIRSMTLRSERNT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FER-1999) to the EMBL/GenBank/DDRJ datahases.
                                                           Saunders S.E., Burke J.F., Benjamin P.R., multimeric CREB binding sites in the promoter regions of a family of orphan G-protein coupled receptors related to the vertebrate galanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 RTIIFALLVAVCLVGFVGNLCVIGILLHNAWKGKFSMIHSLILNLSLADLSLLFSAPIR 82
                                                                                                             PROSITE; PS00217; G_PROTEIN_RECEP_F1_1; 1.
PS502Cf; G_PROTEIN_PECEP_F1_2; 1.
G-protein coupled exceptor; Glycoprotein; Receptor; Transmembrane.
SEQUENCE 380 AA, 42723 MW; D5455BE29BFE4EC4 CPC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 WFAILLIWIIILCGNTFILLQFGVFNYVHEGENRSACL-NLKELKEHEAGKAFFGSFLFF
                                                                                                                                                                                                                                                                                                                                                                                    DB 5; Length 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sia G.M., Maggio J.E., Too H.P.; "Construction of a functional EGFP-tagged avian substance P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   328 NFRESFRELCCIESSRRMEYERTNVRFTVIEK-ETTTITKGICVINISK 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---- KWMITKEPTVSESCETPACNSE 331
                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 12 6%; Prod No 1 20-10;
nes 79; Conservative 69; Mismatches 142; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    10.7%, Score 232.5; DB 5
:: A%; Pred No 1 2e-10;
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                                                                                                                                                                                                                           InterPro; IPB000276; GPCP_Phodpsn
                                                                                                                                                                                                                                                           PRINTS; PRO0237; GPCPPHODOPSN
PRINTS; PRO1570; NPFFRECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken)
                                                                                                                                                                                                                                                Pfam; PF00001; 7tm 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  299 EFREGLKGVW
Lymnaeidae; Lymnaea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                             HSSP; P02699; 1BOJ.
                                                      SEQUENCE FROM N.A.
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                NCBI_TaxID=6523;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  194 J. F. PLIAPGIPIEFFFASFYPWBAYFGGPFYBGTPTGULRHGTRSPGVTVMILSTAIIS-AL 24R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             208 TYFLFLEUVIGGAYTVVSITUWAS----ELPGDSSUPYHEQVSAKPKVVKMMIIVVGTFÄL 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            · · · · PEWVAWLWVWHLFAAGPAPPQGFIALSQVLMFSISSAMPLIFLVM 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81 IPATAYSKSUWDLGWFUCKSSDWFIHTCMAAKSLTTUWUAFUCFMYASDPAFQUSIHNYT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         141 [WSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEEFMSMFGKLY----- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             151 TKVVICVIWIJAFIJAFPQGYYSVTEBLPGFLVCLVAWP---EHSTRVYGKTYHFCMTVI, 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ONVINAVMUAM SSTMYRPITY OF ALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 WPTITPAL-LVAVCLV3PVSNLCVTGITLHNAWESRFSMTHSLILNLSLAGLSLLESAP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --- SIMILARITY- RELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gavia porcellus (Guinea pig)
Bukaryota, Metaroa, Chordara, Craniata, Vertebrara, Eureleostomi,
Mamonilia, Eithoria, Fodenia, Hystricoguathi, Cavidae, Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                         Sporty Match
Best Local Similarity 24 1%; Prod No 20-10;
Matches 92, Conservative 50; Nismatches 142, Indels 57,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.6%, Score 230, DB 11, Length 440, 24 6%; Pred No. 2 38-10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 AA; 49516 MW; FR48B93F595454D9 CPC64;
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01-DEC-2001 (TrEMBLrel: 19, Last sequence update)
01-MAP-2002 (TrEMBLrel: 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  297 SEEFFEGILKGVWFWMTTKKPPTVSESQETPAGNSEGLPDK 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             313 NDRFRVGFKHAFRWC-----PFVS-----AAEYEGLEMK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44? AA
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                          EMBL, AF131057; AAD31017.1; -.
HSSP; P29274; 1MMH.
InterPro; IPF000776; GPCE_Phodpsn.
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Rest Local Similarity
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22 WETTIFALLY AVTLYSFYSNETVISILLHNAWKGKPSMIHSLILNLSLADLSLLLFSAP 80

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81 IPATAYSESUMPLIMEUPESIMETHTPMAARFITIUUMAKUTEMYKSITERE 1800 109
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                                                                                                                                                                                                                                     11.6. WHEYALHGEWYETANY PETAFERTAVERSTAN STATISTICS (1971) 17.5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 IPATAYSKSVWPLGMEVÇKSSFWFIHTGMAARSTTIVVVAARVGRMYASDIAR LVCHBY LGG
58 WEVALMSLAYGAVVAVAVLONILYVIMIVI. - AHPPMPTVTNSFF VIV. RAFALANA AARAF. VAL. 115.
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- SURGELUIAR LINATIN INTERAL MYMFARN FRITTY BY TAXIBLE INTERACTION OF SUBMITMENTAL BREADAST TO FAMILY LOF G PROTEIN ACTURE PROFIT BEST BREADASTAL ARPS33341 AAP62517.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 PLLMPURIEFASEVEMEAV OG-PYROTOFIQUADAJAR PLUMATURATURATURA PROBLEMATOR PROB
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HSSP, MSI A226A; Tacr3.
MSD, MSI A226A; Tacr3.
InterPro; IPP000276; GPCP_Phodpsn.
PRAM, PP00001, 7Lm_1; I.
PPINTS, PP000017; GPPPH0P0PSN
PPSITE; PS60277; GPPPH0P0PSN
PPSITE; PS60277; GPPPH0PNFN
PPSITE; PS60277; GPPPH0PNFN
SEQUENCE A55 AA; 51026 MW; 7A46D400AD7F0444; PP.44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Feild J.A., Brun K.A.; "Molecular cloning and characterization of the marine near kinns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Merazoa, Chordata, Craniata, Vertobratu, Eutologo ed
Mammalia, Eutheria, Eggeria, Grint graffi, Vertie, Mageria, Mo
NCRI TaxiD=10090;
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10.5%; Secre 22%; DR 11; Torin's 48
Best Local Similarity 23.3%; Pred. 35, 3.56+10;
Matches 90; Conservative 63; Mismatches 161; Todolo
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Last annotation update
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187 WLPYHIYETITAIN<sub>UMU</sub>UBEWEYI :
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Q9VAU0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 10.5%; Score 227; 28 11; Lergth 422; Best Local Similarity 24.3%; Pred. No. 3.9e-10; Matches 99; Conservative 63; Mismatches 164; Indels 82; Gaps
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194 FILLAFGLELEFASFYFWSAY----QQCKKRGTKTQWLRWQIRSKQVTVMLLSJALIS-ALL 243
                                 246 PLLIMGVTYTIVGITLWGGEIFGDTCDK-----YHEQLKAKRKVVKMMIIVVVTFAIC 298
                                                                  250 WIPEWY-----AWLWVWHIKAAGPAFPQGFIALSQVLMFSISSANPLIFLVMS 297
                                                                                                   299 WLPYHVYFILTAIYQQLNRWKYI------QQVYLA-SFWLAMSSTMYNPIIYCCLN 347
                                                                                                                                                                        348 KRFPAGFKRAFPWCPFIQVSSYDELELKTTPFHPTPQSSLYTVSPMESVTVLYDPSEGDP 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Mētazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rođentia, Sciurognathi, Muridae, Murinae, Ratlus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 HFAGGTLPSDSQEW------RTIIPALLVA---VCLVGFVGNLCVIGILLHNAW 53
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21555362, PubMed=11698613, Many D. Herman T. Prichard L. Mang D. Herman T. Prichard L. M. Spitzer P. H. Ahlbrand R. L., Kramer G. L. Perty F. Sallee F. P. Richtand N.M.; "Cloning, expression, and regulation of a glucocorticoid-induced receptor in rat brain: effect of repetitive amphetamine."; J. Manteser 21 and 27562601. EMBL; AV629671, AAK29494 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412 AA; 47957 MW; 4917CA9C33A8BFE9 CRC64,
                                                                                                                                                                                                                                                                                                                                                                   01.MAR_2002 (TrEMBLrel. 29, Greated)
01.MAR-2007 (TrEMBLrel. 2), Last sequence update)
01.JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glucoconticoid-induced receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS, PROGLYT, GROWBINDOESH.
PROSITE, PSOCLET, G-PROWBIN RECEP_P1_1; UNENOWN_1.
PRUSITE, PSSC.61, G_FF.GEIN_PBOCKP_F1_1, 1
                                                                                                                                                                                                                                                                                                                                    422 AA
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                                                                                                                                                                                                                                                                                                                                    PPELIMINAPY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SECUENCE FROM N A.
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                                                                                                                                                                                                                                                                                                                                                      08VHD7;
                                                                                                                                                                                                                                                                                                                                  Q8VHD7
                                                                                                                                                                                                                                                                                                RESULT 9
                                                                                                                                                                                                                                                                                                                   Q8VHD7
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EMBL, AJ270459, CAP77262.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83 ATAYSKSVWPLOWPVCKSSDWPIHTCMAAKSLTIVVVAKVOFMYASPPAKQVSIHN YII 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metadoa; Mcllusca; Gastropoda; Pilmonata; Basommatophota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 ELİVETIFGYLÇILƏLEGNƏLVILAVVSE FAMPNITANILİLƏLAVABLLEILEÇVERT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 WSVLVAIWTVA... SLLPLPEWPFSTIRHHEGVEMCLVDVPAVAEE....FMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 WEALPLIWITLEGROOPTLIQEGVERNVHEGENEGACL REKELFERERATERESFLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 2%; Score 220 5; DB 5; Length 380; 22.2%; Pred No. 1 16-09;
323 MALYFARHWERMSSICHNPEINCWENENFRUELMALLS MODRF CHROE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299 EFRECLEGUEGVW-------KWMITKEPPTVSESQETPAGNSE 331
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                                                                                                                             PRIISPVPEFRVAWTEPSHGFRALLANHHIPSSOIGSSPTDLSSV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PSS0262, G PROTEIN RECEP F1_2; 1.
G-protein coupled receptor; Peceptor.
SEQUENCE 380 AA, 42773 MW, DPB1ES6A20C72629 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUM-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                   380 AA
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                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lymnaea stagnalis (Great pond snail)
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                                                                                                                                                                                                                                                                                                PPT;
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HSSP, P02699, 1BOJ.
Interpro, IPP000274, GPCP Phodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAM, PF00001, 7tm 1, 1.
PRINTS, PR00237, GPCPRHODOPSN.
PPINTS, PR01570, NPFFPRCEPTOP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G-protein coupled receptor.
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                                                                                                                                                                                                                                                                                                   PPELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
es 78; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lymnaeidae; Lymnaea.
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141 VARBEMS MEGRINALISERSERIEFAGETYWRATYGGYRE """""" 1957 B.T.C. O.
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Biochem. Biophys. Ros. Commun. 273:571-577 (2000);
Biochem. Biophys. Ros. Commun. 273:571-577 (2000);
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Interpre, Ippnonion (APPR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metaria, Arthropida, Traehoata, Hoxup, Li, Liberte, Prerygota, Mongeera, Endopterygota, Diptera, Bruchymota, Kirlepydroida, Drosophilidae, Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 AKQVSIHNYTIMCYLVAIWTVAGLIPIPPEMPPOTPPHHPPROPPOTTVPA
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6) orf.ppec (TrEMBLre) 15, Created' of port 2000 (TrEMBLre) 15, Last sequence updated of drema-2002 (TrEMBLre) 20, Last amonation updated
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PRINCE, PROTOCO, NEPRESCROTOR,
PRODUCT, AS TERM, TOWN II I TWENKEW,
PROSITE, PROTOCO, AS TERM, TOWN II I TWENKEW,
PROSITE, PROTOCO, AS TERM, TOWN II I TRANSMIT
FROSITE, PROTOCO, AS TERM BRIEF II Z, II.
PROSITE, SOURCE, AS TAN, 40646 MM, 2624074446224704
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Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                          Receptor.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                       Lundell I., Boswell T., Larhammar D.,
"Chicken Neuropeptide Y Family Receptor Y4; a Peceptor with Equal
Affinity for Pancreatic Polypeptide, Neuropeptide Y and Peptide YY.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
PMRI, AF410RE3, AAL84161 1;
                                                                                                                                                                                                                                                                                        Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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194 FTTUDFLOPPTYQVTFF1SSY1J.PLM11SGLYMPMIMPLWPQGTGVRMSKESQRGPKRVT 255
                                                      256 RLVVVVVIAFÄSLWLFVQLILL....LKSLDVIETNTLTKLVIQVTAQTLAYSSSCINFL 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     251 LPEWVAWLWV-WHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEFREGLKGV 307
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                           23.7 VMLLSIAIISALLWLPEWVAWLWVWHLKAAGPAPFQGFIAL·····SQVLMFSISSANFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 377;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 AA, 42372 MW, C9RCECOODBED1F3E CRC64,
                                                                                                                                                                                                             01-07N-2002 (TrEMBLrel. 21, Created)
01-07N-2002 (TrEMBLrel 21, Last sequence update)
01-07N-2002 (TrEMBLrel 31, Last annotation update)
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Last annotation update)
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01-MAR-2002 (TrEMBLrel. 21, Last seq
01-JUN 2002 (TrEMBLrel. 21, Last and
Allatostatin receptor RAP
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                                                                                                                                                                                      PPT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68; Conservative
                                                                                                                                                                                      PRELIMINAPY;
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                                                                                   292 IFLUMSEEFRE 302
                                                                                                             312 LYAFLSENFRK 322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                   Gallus
NGBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Q8QGM3
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SERUTENCE FROM N A STRAIN-LYON 200 BA/LYON 300 AB; STRAIN-LYON 200 BA/LYON 300 AB; SEDAIN-21601656; FubMed-1150150; Secher T . Lenz C . Cazzamali G., Sorensen G . Williamson M., Hansen G.N., Syane P., Grimmelikhuijzen C.J.P.; "Molecular Cloning of a Functional Allatostatin Gut/Brain Receptor and an Allatostatin Freprohormone from the Silkworm Bombyx mori."; Diebl. AF303370; AAL47055-4705011
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 AYSKSVWDLGWPVGKSDWFTHTCMAAKSLFTVVVAFVGFMYAGTFAFQVSTHWYTTWOV 144
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O'Carroll A -M.;
"Cloning, sequence and rissue distribution of the gene encoding a mouse sometostain subtype 5 receptor.",
Submitted (MAY-2000) to the RMRL/GenPank/DDBJ databases.
-! SURCELDUAR LOSATION INTEGRAL MEMBRANE PROTEIN (BT SIMILARITY).
-! SIMILARITY. BELONG TO FAMILY 1 OF GIESTEIN COUPLED RECEPTORS.
BMBL, AF268067; AAF72547.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 IIPALLVAVCLVGFVGNLCVIGILLHNAWKGKPSMIHSLILNLSLAFLSLLLFSAPIRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 LVA---IWTVASLLPLP-----EWFFSTIRHHEGVEMCLVDVPAVAEEFMSMFGKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 LLÁIACIWVVILTTAIPVGICHGERÉYSYFNRNHSSCV-------FLEERG--Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     194 PILAPGIPIEPASP ----- YEWRAYDGCYRRGIKIGNIRNGIRGYCHONDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         205 SKLGPQMSFFLSSYVIPLALISVLYMOMITPLWFSAFGGVSARSPRGP. FFVTRMIN
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Mammalia, Euthoria, Podentia, Sciurgnathi, Muridae, Virinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.9%; Score 214.5; PB 5; Length 361;
14.6%; Pred No 2.20.09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 6%; Pred No cr way tive 52; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 AA, 40478 MW, 63C2B2846FC3010A CRC64;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01 MAP.2002 (TrEMBLrel. 20, Last annotation update)
Somatostatin subtype 5 receptor.
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PRINTS, PR00237, GPCREHODDEN.
PPOSITE, PS00239, AA TPNA LIGASF II 2, THYNOWN 1.
PPOSITE, PS00237, 3 PFOTEIN RECEF FI 1, THYNOWN 1.
PPOSITE, PS00222, 3 FFOTEIN RECEF FI 1, THYNOWN 1.
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EMBL, AF303369; AAL47056.1; JOINED.
EMRL, AF304442; AAG4431.1
InterPro, IPPO/2106; AAPNA ligasell.
InterPro; IPPO/276; GPOP_Phodesn.
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HSSP; P02699; 1F88.

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             InterPro; IPR000276; GPCR_Rhodpsn.
Priam; PR00001; 7rm 1; 1.
PROSITE; PS00237; GPCRHPDOFSN.
PROSITE; PS00237; GPROTEIN_PFCEP_F1_1; 1.
PROSITE; PS00237; GPROTEIN_PFCEP_F1_2; 1.
G-PROSITE; PS00237; G-PROTEIN_PFCEP_F1_2; 1.
G-PROSITE; PS002424; G-PROTEIN_PFCEP_F1_2; Non-PFCPT Transmembrane
SEQUENCE ANS AA; 44449 MW; Non-PFCEP_F1 Transmembrane
                                                                                                                                                                                                                             51;
                                                                                                                                                                                 Ouery Match
Rost Local Vimilarity 24 O%; Prod. No. 3 40-09;
Matches 89; Conservative 67; Mismatches 164; Indele 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                      125 MYASDPAKQVSIH NYTIWS
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Search completed: January 28, 2003, 11:51:30 Job time : 38 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

January 28, 2004, 11-49-21, Search time 21 Seconds (without alignments) 1858.599 Million cell updates/sec Run on:

US-09-828-432-3 Perfect score: Title:

1 MNVSFAHLHFAGGYLPSDSQ.

.....QDNDPIPWEHEDQETGEGVK 406

**BLOSUM62** Scoring table: Sequence:

283224 seqs, 96134422 residues Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters.

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		* Query				
No.	Score	Match	Length	DB	ID	Description
, , , ,	1 10 11	. (1	တ	C1	JC5949	galarin receptor 2
C 3	6.1	ci	349	C 1	5933	cept
~	236.5	0	- 1	C)	4047	Soi
4	236	Ö	444	C1	$\alpha$	hypothetical prote
'n	231	Ö.	407	CI	2351	neurokinin 1 recep
S	600	Ċ,	419		522	
7	227	9.	P: 07		343	e-4
œ	227	L)	407	C1	030	neurokinin 1 recep
6	2.4.5	. ,	440		9	opi
10	224		465		0151	3
11	223.5	0	443		4047	coic
1.2	221		395		S55524	neurokinin 3 recep
13	221	Ö	407		1.1	neurokinin 1 recep
14	221		452		CD.	in 3
15	218		357		JC7319	$\overline{}$
16	217		363		10	angiotensin II rec
17	216 5	10 0	390			bombesin receptor,
18	216.5		402		156595	CI
19	215.5		384			
20	215.5		390			C)
ci	214	,	363			angiotensin II rec
c1 C1	214	9.9	384		520303	neurokinin 2 recep
23	211.5		375		8	neuropeptide Y/pep
4.0	211	0	16.3		6	angiotensin II rec
25	210 5	0 7	αρξ		5	neurokinin 2 recep
97	208.5	9.6	375		302300	pancreatic polypep
C1	90		444		8	
82	0	٠.	428		305	13
2.9	206.5	9.5	431		C40470	glucccorticoid ind

205.5		384	C1	I57957	peurokinin 2 recep
205	ω. Ω.	436	C-1	0688DD	cholecystokinin-A
04.5		391	C1	A41795	somatostatin recep
34.5	9.4	391	C1	C41795	somatostatin recep
204.5	9.6	391	C1	A39297	somatostatin recep
204	9.4	428	C1	A44021	somatostatin recep
203.5	4.	372	C1	B48227	delta opicid recep
203	9.4	363	C1	IS7940	somatostatin recep
203	9.4	394	C1	JC7209	galanin receptor -
203	9.4	420	C1	151666	Mel-10 receptor su
202.5	9.3	391	C I	T32517	hypothetical profe
202	9.3	413	C I	JN0692	cholecystokinin ty
2007	9.3	372	C1	138532	delta opicid recep
198.5	رة د.	519	C4	S17783	tachykinin recepto
97.5	9.1	430	C 1	I51898	cholecystokinin A
196	0.6	328	c٩	I38973	G protein-coupled

# AL.IGNMENTS

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galani receptor 2 - human
C;Species: Homo sapiens (man)
C;Accession: UC5949 #sequence_revision 16-Jul-1999 #text_change 21-Jul 2007
C;Accession: UC5949 Beauchamp, M.R.; Zhelnin, L.; Brown, S.E.; Gore-Willse, A.R.; Gregor, R;Bloomquist, B.T.; Beauchamp, M.R.; Zhelnin, L.; Brown, S.E.; Gore-Willse, A.R.; Gregor, Biochem. Biophys. Res. Commun. 243, 474-479, 1998
A;Title: Cloning and expression of the human galanin receptor GalR2.
A;Reference number: JC5949; MUID:98153789; PMID:9480833
                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GB:AF040630; NID:g2921759; PIDM:AAC29634.1; PID:q2921740
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C.Species: Homo sapiens (man)
C.Date: 31-May-1996 #sequence revision 31-May-1996 #text_change 21-Jul 2007
C.Accession: 159336; "Grafol; G01765; G02528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187 S... MEGKLYPLLAFGLPLAFGFYFWPAYDQCKKRGTKTQMLPNGTRSKQVTVMLLST 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243 AIISALLWLPEWVAWLWWWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEFRE 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.7%; Pred No 1.39-13;
Matches 85; Conservative 53; Mismatches 154; Indels 26; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             II GGYLPSDSGEWFIIIPALLVAVCLVGPVGNLGVIGILLHNAWFGYPFWFHSLINN SLAD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 DICTEVESYLLEVLVLGLTYARTLRTLWFAVPV-AAGGGAFFAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: vertebrate rhodopsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 GLKGVWKWMITKKPPTVS 320
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                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-387 <BLO>A;Closs-referent
                                                                                                                                                                                                                                                                                                    A;Accession: JC5949
A;Status: preliminary
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A;Reference number: A40470; MUID:92123228; PMID:1663214
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A, Accession: T27866
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                                      A, Accession B40470
A, Status: preliminary
A, Molecule type: mRNA
A, Pesidues: 1-423 < HAR>
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A, Intrens. 19/1, 1
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A.Molecule type: mRNA
A.Residue: prediminary, translated from GB/EMBL/DDBJ
A.Molecule type: mRNA
A.Residue: page: mRNA
A.Press treferences GB L34342, RID g860447, FITN:AAA807671, FID:g559048
B.Lorimer, D.D.; Matkowskj, K.; Renya, P.V
B.Lorimer, D.D.; Matkowskj, K.; Renya, P.V
B.Lorimer, D.D.; Matkowskj, K.; Renya, P.V
A.Title: Cloning, chromosomal location, and transcriptional regulation of the human gala A.Reference number areas, mulliples of the human gala A.Reference number areas, mulliples and sequence not shown
A.Reference number areas, and sequence not shown
A.Residues 1.340 (LGE)
A.Residues 1.340 (LGE)
A.Residues 1.340 (LGE)
A.Residues are references GB-HRASHI; NID-g1297337; FIDN:AACHORS 1, PID-g1297338
A.Residues are references GB-HRASHI; NID-g1297337; A.Reference submitted to the EMBL Data Library, April 1996
B.Ross, P.C.
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B.Ross, P.C.
B.Ross, P.C.
B.Ross are references GB-HRASHI; NID-g1297337; A.Reference submitted to the EMBL Data Library, April 1996
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A;Accession: G01765
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E.Harrigan, M.T., Tapkell, M.F., Rangelis, J.
Mol. Endocranol. 5, 1331-1338, 1991
AyTitle: Identification of A gene induced by glucocorticoids in murine T-cells: a potent
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C;Species: Mus musculus (house mouse)
C:Date: [4-Feb-1992 #sequence_revision 14 Feb 1992 #fext_change 20-Apr.2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95 WEVÇESSDWEJHTCMAAKSLTIVVVAKUCEMYASEFAKQYSI-HNYTIWŞVLVA---- 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 - LAFG--LPLFFASFYFWPAYDQCKKPGTKTQNLPNQIPSKQVTVMLLSIAIISALLWLF 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 EWVAWIMVWHIKAAGPAPP@GFI--ALSQVIMFSISSANPLIFLVMSEEFREGLKGVWKW 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204 TEVERYLIPILLITERYAPVINHIHEY-LENMSPPSEASFFFTAGTVILVVVVPGISWLD 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 HHIIHLWAEF--GVFPLTPASFLFRITAHCLAYSNSSVNPIIYAFISENFPVAYKQVFPC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36 VGFVGNLCVIGILLHNAWKGKP-SMIHSLILNLSLADLSLLLFSAPIRATAYSKSVWDLG 94
R;Habert-Ortoli, E.; Amiranoff, B.; Loquet, I.; Laburthe, M.; Mayaux, J. Proc. Natl. Acad. Sci. U.S.A. 91, 9780-9783, 1994
A;Title: Molecular cloning of a functional human galanin receptor.
A;Reference number: 159336; MUID:95024044; PMID:7524088
A;Acression. 159336.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  321 HI-REDSHLSDTKENKS-----RIDTPPS 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GDB:392699; OMIM:600377
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                                                                                                                                                                                         A; Arcession.
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C,Genetics:
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A;Pesidues: 1-423 «HAR»
A;Cross-references: GB:M80481; GB:M80510; NID:q1935/ic; Flin:AAA.2444...; Flin:Hard Cir
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A)Experimental source: clone 28455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein ZK455.3 - Caenorhabditis ologans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct:1999 #sequence_revision 15.0ct 1999 #rext chapte 25 Apr 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HING ALSQVIME: -- SISSANPI FELVMSEEPPP FIRMWHWM TRHITTORIGHELET AND HOLD AND ALSQVIME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOW TOPPING 46.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 N-----QFMHSATSLFIVNLAVAPIMITHLNTFFTLVPFVVVVVVVV PARMYTVLFFTVVFFVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 FRG - TKTONLENOTESKOVTVMLLSTATISALIMI PEWVANI WVWIT WAA TGATAS TELEVIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45. TEPTEAUTILVOLVOLVALIVITAROPONE SCHWELLIGGARGEMENT CONTENTATOR FOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    153 CSLHVSALTLTAIAVDRHQVIMHPLKPRISITKGVIY- IAVIWVMATFFFGFFGFGALT. (1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          211. PTERYSEDIVESLOTEPEPACI FWRYLCIATETT YTTE TOTAN TANDOTT SELWON STOLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 IIPALLVAVOLVSFYSNLOVISIIJARANESKRSMIHSLILNISLÄKLISLILNESKALIEKT #4
                                                                                                                                                                                                                                                                                                                                            PTIIPALLON WOT WORKS WIND TALLER FOR
                                                                                                                                                                                                                                                                                                                                                                                                                   39 ASSHEWANTIESENGMEVBEEFYBAET DETTVEALLIGENTEETING TORING TOTAL OF THE
                                                                                                                                                                 10 4%, Georg Merch 10 4%, George 236 4, GEO, George 19 Pest Logal Similarity 24 4%, Pred No. 2.86-11;
Marches 101, Conservative 60, Mismatches 174, Indels 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . . .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 STIRHHEGV--EMCLVDVPAVAEEFMSMFGKLYPDJAFGLFLFFASFFFWWAYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TIGENTTEQYLALEPPYPTTYWAXALAWIEALCWEP ... LNCTVITTERA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                329 NSEGLEPPVP - - - - - GPECPA-TFFYFYPOTGOGGGRANDRABI FIL (?)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            370 GEDRIPSPVPSFRVAWTEKSHGRRAPLPNHHLDSSOIG SCHTDLSSVELVV 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122/11, 194/4, 110/0, 100/0, 204/3, 451/1, 4000
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24.8%; Pred. No. 3.36-11;
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Matches 84; Conservative 60; Mismatches 127; Indele
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                                                                                C; Superfamily: neurokinin 1 receptor
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R;Gorbulev, V.; Akhundova, A.; Luzius, H.; Fahrenholz, F.
Biochim. Biophys. Acta 1131, 99-102, 1992
A;Title: Molecular cloning of substance P receptor cDNA from guinea-pig uterus.
A;Reference number. 323510; MUID:92256498; PMID:1374648
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C;Superfamily: neurokinin 1 receptor
C;Superfamily: neurokinin 1 receptor
C;Reywords: G protein-roupled receptor; glycoprotein; transmembrane protein
F;32 55/Domain: transmembrane #status predicted <TML>
F;69-89/Domain: transmembrane #status predicted <TML>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurokinin 1 receptor - guinea pig
N;Alternate names: NK-1 receptor; substance P receptor
C;Species: Cavia porcellus (guinea pig)
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 19-May-2000
C;Accession: S23510; S19198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              204 IYFLPLLVIGYAYTVVGITLWAS----EIPGDSSDRYHEQVSAKRKVVKMMIVVVCTFAI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 LWLPEWVAWLWVW-----HLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEBFREG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ...----wmitkkpptvsesQetpagnseglpdk 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 FMMAFRCCPFISAADYEGLEMKSTRYFOTOGSVYKVSPLETTIS----TVVGAHEEDPBE 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141 IWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEEFMSMFGKLY----- 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 ----PLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLLSIAIIS-AL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260 CWLPFHIFFLLPYINPDLYLK---KFIQQVYLAIMWLAM-SSTMYNPIIYCCLNDRFPLG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 IRATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSIHNYT 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 VIETYAVIINEWYYGLFYCKFHNFFPIAAVFASIYSMTAVAFDRYMAIIHPL-OPRLSATA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147 TKVVICVIWVLALLLAFPOGYYSTTETMPGRVVCMIEWPSHPDK---IYEKVYHICVTVL 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80; Mismatches 159; Indels 64; Gaps
                                                                                                                                                                                                                                                                                                                                                                                  --SKQVTVMILSIAIISALLWI,PEWVAWLWVWHLKAAGFAPPQGFI------275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 WRTIIPALLVAVTLV-GFVGNLCVIGILLHNAWKGKPSMIHSLILNLSLADLSLLFSAP 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30 WCIVLWAAAYTVIVVTSVVGNVVVMWIIL--AHKRMRTVTNYFLVNLAFAEASMAAFNTV 87
                                                                                                                                                                                      FM--SMFGKLYPLLAFGLPLFFASFYFWRAYDOCKKRGTKT---ONLRNQ----IR--- 231
                                                                                                                                                                                                                                                                                  215 PMTFNVFGYVLPL---GISVVLYGLMLRKLWDMPRPGNSQSVGGRNLTNRDSGSSIRRRP 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 EATAARPRVIPLULOULITWALCWLPLNVOFF-----MSGLAYPEPLVISHGVIMVIVQ 325
--EGVEMCLVDVPAVAEE----- 184
                                                                                                162 ALCFIYIIIIASOIPVG-----RMHGIYVYDFIMEKRSTCAILTIATAEATPTMARTY 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10.7%; Score 231; DB 2; Length 407; 22.1%; Pred. No. 7.3e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F)17-128/Domain: transmembrane #status predicted <TM3>F)149-169/Domain: transmembrane #status predicted <TM4>F)169/Domain: transmembrane #status predicted <TM4>F)250-280/Domain: transmembrane #status predicted <TM5>F)250-280/Domain: transmembrane #status predicted <TM5>F)250-280/Domain: transmembrane #status predicted <TM6>F)250-280/Domain: transmembrane #status predicted <TM6>F)250-280/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F)260-200/F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 IAŻŻVLAYTNŚCLNPILYALMSQSPPEGFIPVMKMLINK 364
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                    142 WSVLVAIWTVASLLPLPEWFFSTIRHH--
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A; Residues: 1-407 <GOP>
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Files augustic transmembrane mouter. (Sovalent) #Statum yer.
Files 9316/Domain: transmembrane (Ash) (covalent) #Statum yer.
Files 917,30/Binding site: carbohydrate (Ash) (covalent) (by protein kinase C) #status Files. Priles 1917,312/Binding site: phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict Files. Phosphate (Ser) (covalent) (by cAMP-dependent kinase) #status predict Files in the phosphate (Thr) (covalent) (by protein kinase C) #status predicted
                                                                                                                                                                                              somatostatin receptor 3 - human ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("Species: Homo sapiens (man) ("Species: Pepper) ("Basquence_revision 18 Nov 1334 #text_change 24 Nov 1939 ("Accession: A46226, 53250] ("Paymada, Y.; Relsine, T. Law, S.F., Thara, Y.; Embota, A.; Ragimoto, S.; Seino, M.; Seino, M.; Badoorinol, 6, 2136-2142, 1932 A, Title: Somatostatin receptors, an expanding gene family, cloning and functional charact A; Reference number: A46226, MUID:93149123; PWIP:1337145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Title: A human somatostatin receptor (SSTR3), located on chromosome 22, displays prefer
A,Reference number. S32501; MUID:93238970; PMID:8097479
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C;Keywords: G protein-coupled receptor, glycoprotein; phosphoprotein; transmembrane proff
F;44-70/pomain: transmembrane #status predicted <PML>
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A;Note: sequence extracted from NCBI backbone (NCBIN:123685, NCBIP:123690)
R;Corness, J.D.; Demchyshyn, L.L.; Seeman, P.; van Tol, H.H.M.; Srikant, C.F.; Kent, G. FEBS Lett, 321, 279-284, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 IIPALLVAVCLVGFVGNLCVIGILLHMAWKGKPSMIHSLILMLSLADLSLLLFSAPIRAT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 LIPLVYLVVCVVGLLGNSLVITVVLRHT--ASPSVTVVYLLNLALAD ELFMLGLPFLAA
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tive 63, Mismatches 160, Indels
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372 GPK-ATPSSLDLTSNGSSRSNSKTVTESS 399
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A;Introns: #status absent
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A;Molecule type: DNA
A;Residues: 1-418 <COR>
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Nalternate names: NK-1 receptor; substance P receptor
C)Species: Mus musculus (house mouse)
C)Date: 22-Nov 1993 #sequence revision 10 Nov 1995 #text change C, Bun, 180
C)Date: 22-Nov 1993 #sequence revision 10 Nov 1995 #text change C, Bun, 180
C,Accession S20304; T67216, T304
A)Tille: Molecular S20304
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C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun 1994 #text elanor .2 Apt .5.ee
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Cisuperfamily: neurokinin I proceptor
Cisuperfamily: petrolein-roupled proceptor; transmembrane pictors.
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Bost Local Similarity 22.6%; Pred. Mr 1.56-10;
Matches 88; Conservative 72; Mismatches 165; Indels
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A,Status: proliminary, translated from on/EMRL/DDR.
A,Molecule type: mRNA
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            - mouse
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neurokinin 1 receptor
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Characterian ARRADIAGE TOWERS TO 22. Jan. 1903 #Fext_change 19.May.2000

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J. Biol. Chem. 266, 4366-4344, 1991

A. Fillel Organization, Structure, and expression of the gene encoding the rat substance A. Fillel Organization, Structure, and expression of the gene encoding the rat substance A. Fillel Organization, Structure, and expression of the gene encoding the rat substance A. Fillel DMA.

A. FRESIDIAGE TO A. TANATAS.

A. FRANCESSION ARAJEST TO A. TANATA, WITD 91154239; PMID.1705552

A. FRANCESSION ARAJEST TO A. TANATA, MATD A. F. FILLEL CO. TANATAS.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 IMIPEWVAWIWVW-----HLKAAGPAPPOGFIALSQVIMFSISSANPLIFLVMSEEFREG 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 FKHAFPCCPFISAGDYEGLEMKSTPYLQTQSSVYKVSPLETTIS----TVVGAHEEEPEE 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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      326 ----RVLLRPSRRVRSQEPTVGP----PEKTEEEDE----EEEDGEESREGGKGK 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 407,
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22.9%, Fred, No. 1.5e.10;
tive 71; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                        neurokinin 1 receptor - rat
N.Altermate names NY 1 receptor, substance D receptor
C.Species: Patrus norvegicus (Norwsy rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          337 VPSPESPASIPHKEYPSSPSSGYGKTEKA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    372 GPF ATPSSIDITSNGSSPSNSKTMTESS 399
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C,Accession: A44081 R:Xie, G.X.; Miyajima, A.; Goldstein, A.

RESULT 8 820304 one of

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Cyacession: D40470
R.Harrigan, M.T.; Campbell, N F; Bourgeois, S.
Mol. Endocrinol. 5, 1331-1338, 1991
A; Title: Identification of a gene induced by glucocorticoids in murine T ceilb: a potent:
A; Reference number: A40476, MJID: 92123239; iv: F: tebs214
                                                                                                                                      Cycomenters: 10 1 2019-199126
A gene: 198-170-199-199126
A conserved and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the second and the seco
A/Residues: 1-438,'F',440-465 <TAK>
A/CLOSS-references. GE.XUS172, NIB.375022, FIDM.CAA46291.1; PID:GR25635
C/Comment: The endogenous ligand of this receptor is neurokinin 3 (neuromodin K),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gluccorticoid-induced receptor, long form RP105 - mouse
G;Species: Mus musculus (house mouse)
G;Date: 14-Feb-1992 #sequence_revision 14-Feb-1002 #text_clande 20 Apr 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 NAWKGKPSMIHS----LILNLSLADLSLLLFSAFIRATAYSKSVWDLGWFYCKSSDWFIH 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             233 KQVTVMLLSIAIIS-ALLWLPEWV------AWLWVWHLKAAGPAPPQGFIALSQ 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       294 KRKVVKMMIIVVMTFAICWLPYHIYFILTAIVQQLNRWKYI-----QCVYLA-SF 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 AEBEMS-----MEGKLYPLLAFGLELFFAGEYFWRAY - JULYFFFGIRIONLRAGIRS 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 PKOHFTYHIIVIILVYCFPLLIMGITYTIVGITLWGGEIFGTTCDE-----YHEQLKA 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 PLVNLAFSDASMAAENTLVNFITALHSEWIFGANTCRFÇRFFFTTAVFASITSMIALAVE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 CEMYASOPAK-QVSIHNYTIWSVLVAIWTVASLLFLFEWFFSTIRHHEGYEXCLYDVDAV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 RYMAIDPUKEKLSATATKI.-VISSIWILAFLAFPÇCIYEYTKYRPGRILCFYUWFEC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 AHLHEAGGYLPSGSGDW------ KTITFALLVA- VOLVGFVSKLOVISILLH 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 ASSHFWANTIFSDWONEVGRRRYGAESCHTTVFALLIVANSFTIVFSLFSTHTV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 LILMLSLADLSLLLFSAPIEATAYSKSVWSLGWFVGFSSCWFIHTCMAAKSLTITHTARV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 PAPSQPWANLINGFVQPSWRIALWSLAYGVVVAVAVLGYLIVIWIIL -AHFRMRTVTVY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 PSDSQDWRTII-----PALLVA------VCLVGFVQRLCVIGILLHRRWKGKPSWIHS 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.3%; Score 224; DB 1; Length 465; 23.6%; Pred, No. 3.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62; Mismatches 133; Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 23.48; Fred. No 3 2e-10;
Matches 101; Conservative 61; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 VLMFSISSAMPLIFLVMSEEFPEGLKGVWKW 310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.Cross-references: GB:M80160
C,Superfamily: neurokinin 1 receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 78; Conserva
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A;Residues: 1-443 <HAR>
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A;Title: Molecular characterisation, expression and localisation of human neurokinin-3 r A;Reference number: S20435; MUID:92183914; PMID:1312036
A;Accession: S20435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Title: The primary structure and gene organization of human substance P and neuromedid
A, Reference number S21198, MTP 92201196; PMID-1312928
                     Pro- Ratl Arad Sci U S A 99, 4124-4128, 1997
A;Title: Expression cloning of cDNA encoding a seven-helix receptor from human placenta
A;Reference number: A44081; MUTD.9233319; PMID:1315951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NiAlternate names: neuromedin K receptor; NK-3 receptor
C;Species: Homo sapiens (man)
C;Date: 20.Apr.2000 #ecquence revision 20.Apr.2000 #text_change 19-May-2000
C;Accession. 201517; 220453; 21137
R;Huang, R.R.C., Cheung, A.H., Maxina, K.E.; Strader, C.D.; Fong, T.M.
B;Ochem. B;Ophys. Res. Commun. 184, 966-972, 1992
A;Title: CDNA sequence and heterologous expression of the human neurokinin-3 receptor.
A;Reference number. JOL517; MULD:92246993; PM:N:N:1374246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 DIGMFUCKSSPWPIHTCMAAKSLTIVVVAKVCFMYASDPAK-QVSTHNYTIWSVLVAIWT 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 VACLLPLPEWFFSTIPHHEGVEMCLVDVPAVABEFMS------MFGKLYPLLAFGLPLFF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 LABILLAPPOCLYSYIYVMPGPTLCYVQWPEGSPQHPTYHMIVIVLVYCPPLLINGITYTI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 VGITLWGGEIPGDIGDE -- - YORQUKAKPKVVKMMIİVVVTFAICWLPYHIVFILT 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    127 YFGANYCRFQRFFFLTAVFASIYSMTATAVDPYWAIINPLKPPLSATATRI--VIGSIWI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           285 ASEYEWRAY: ...OOCKPFTFYTGHLRHGIPSKOVTVMLLSIAIIS-ALLWLPEWV...- 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 AVVAVAVLGNLVVIMIVL--AHKRMRTVTNSFLVNLAFADAAMAALNALVNFIYALHGEW 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A,Residues: 1-465 «HUA»
A,Cross-references: GR M83471, NID.g189223, PIDN:AAAR6366 1; PID.g189224
A,Experimental source: brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule Lype: DNA
A,Residues: 1-2,'1',4-62,'P',64-465,<BUE>
A,Cross-references: GB.S86392, MID.9246908; PIDN:AAB21706.1; PID:9246909
R,Takahashi, Fanaka, A.; Hara, M.; Nakanishi, S.
Eur. 3. Biochem: 204, 1025-1033, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 AVCLVGFVGNLCVIGILLHNAWKGKPSMIHSLILNLSLADLSLLLFSAPIRATAYSKSVW 91
                                                                                                                                                                                                               A,Status: preliminary
A,Molecule type: mRNA
A,Molecule type: mRNA
A,Residues. 1-446 <MIS-
A,Cross-references GR M84665, NID.g189321, PIDN:AAA36395.1; PID-g189392
A,Cross-refermily: neurokinin 1 receptor
C,Superfamily: neurokinin 1 receptor
C,Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 24.5%; Pred. No. 2.7e-10;
Matches 74; Conservative 59; Mismatches 124; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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A,Accession: S21237
A,Status: proliminary
A,Molecule type: DNA
                                                                                                                                                                    A;Accession: A44081
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Oy 215 VTVMILSTATIS-ALLWIDEWV AMIWVMBLKAATTATE-FFTALLTO	AyTitle: Molecular cloning, structural characterization and famous according AyEference number: JO1274, MUID: 92628466; PMID: 1716-27  AyMolecule type: mRNA AyMolecule type: mRNA AyMolecule type: mRNA AyMolecule type: mRNA AyCross-references: GBEN74290; NID: 4318612; PIDN: AAAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	A Accession S21188 A Status: preliminary A Molecule type: DNA A Perighes 1407 TAV2. A Prelimes 1407 TAV2. A Cross-references: GB:X6517; NID:q36616; PHNYC/M46. Liling 1. Comment: The endogenous ligand of this receptor is near kind. C Comment: The endogenous ligand of this receptor is near kind. A Gene GB-TACLE A GENE TACLE A MPP position: 2pter-2gter A MPP position: 2pter-2gter C; Superfamily: near-white-oupling frequency glycoprotein, here receptor C; Superfamily: near-white-oupling frequency predicted (TM2) E; 20 cq/Creain: transmembrane fistancy predicted (TM3) E; 10 124/2/Creain: transmembrane fistancy predicted (TM3) E; 10 124/2/Creain: transmembrane fistancy predicted (TM3) E; 10 124/2/Creain: transmembrane fistancy predicted (TM3) E; 114-169/Creain: transmembrane fistancy predicted (TM3) E; 115-128/Bidding site carbibly drave face (Cervalent: fistance
Db 107 TOWARKSITTIVVARVOEMYASDARQUSHNYTIMSVL	RESULT 12 SHESDA neurokinin 3 receptor - mouse (fragment) N.Alternare names neuroscaln K receptor, NK 3 receptor C.Species Mus musculus (house mouse) C.Steries Mus musculus (house mouse) C.Accession: \$5524, 173045 R.Maroteaux. C.Accession: \$5524, 173045 R.Maroteaux. Shorteaux. Approximate preliminary translated from 38/EMBL/DBR3 Approximated types mRNA Approximately translated from 38/EMBL/SAMITRAL 1; PID-94RC780 C/Superfamily: neurokinin 1 receptor C/Superfamily: neuro	

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22.Jan 1993 #seguence_revision 22.Jan-1993 #text_change 19-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 WLPEWV------AWLWVWHLKAAGPAPPQGFIALSOVLMFSISSANPLIFLVMS 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              299 WLPYHVYFILTAIYQQLNEWKYI------OQVYLA-SFWLAMSSTMYNPIIYCCLN 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 INFIYGLHSEWYFGANYCRFONFFPITAVFASIYSMTAIAVDRYMAIIDPLKPRLSATAT 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 TIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEBFMS-----MFGKLY 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 KI--VIGSIWILAFLLAFPQCLYSKIKVMPGRTLCYVQWPEGPKQHFTYHIIVIILVYCF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             194 PLLAFGLPLFFASFYFWRAY---DQCKKRGTKTQNLRNOIRSKQVTVMLLSIAIIS-ALL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 24.9%; Pred. No. 5.3c.10;
Matches 78; Conservative 57; Mismatches 132; Indels 46; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 IRATAYSKSVWDLGWFVCKSSPWFIHTCMAAKSLTIVVVAKVCFWYASDPAK-QVSIHNY 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 LWLFEWVAWLWWW-----HLKAAGPAPPQGFIALSQVI.MFSISSANPLIFLVMSEEFREG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 FKHAFRCCPFISAGDYEGLEMKSTRYLQTQGSVYKVSRLETTIS----TVVGAHBEEPED 371
                                                                                                                                                                                                                                                                                                                         147 TYVVICVIWVLALLIAFPOGYYSTTETMPSRVVCMIEWP---EHPNKIYEKVYHICVTVL 203
                                                                                                                                                                                                                                                                                                                                                                                        194 ---- PLLAFGLELEPASFYFWRAYDQCKKRGTKTQNLPNQTPSKQVTVMLLSIALIS-AL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 IYFLPLLVIGYAYTVVGITLWAS----EIPGDSSDRYHEQVSAKRKVVKMMIVVVCTFAI 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               260 CWLPPHIPFLLPYINPDLYLK. KPIOQVYLAIMWLAM-SSTWYNPITYCCLNDRFRLG 315
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                                                                                                                             91 IRATAYSKSVWDIGWPVÇKSSDWPIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSIHNYT 140
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                                                                                                                                                                                                                                                           141 IMSVLVAIWTVASLLPDPEWFFSTIRHHEGVEMCLVDVPAVAEEFMSMFGKLY----- 193
22 WRTIIPALLVAVCLV GFVGNLCVIGILLHNAWKGKPSMIHSLILNLSLADLSLLLFSAP 80
                                         30 WOIVLWAAAYTVIVVTSVVGNVVVMMIIL--AHKRMRTVTNYFLVNLAFAEASMAAFNTV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A)Residues: 1.452 - SHI.>
A)Cross-references: 38 005181, HIP-g205470, FIDM-AAA41688 1: PID:g205671
C)Superfamily: neurokinin 1 receptor
C)Reywords: 3 profein-coupled receptor: glycoprotein; membrane protein
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R;Shigemoto, R.; Yokota, Y.; Tsuchida, K.; Nakanishi, S.
J. Biol. Chom. 265, A53.454 1990
A,Title. Cloning and expression of a rat neuromedin K receptor CDNA.
A,Reference number. A34915, MILE 20110113, PMID 2153106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neurokinin 3 teceptor rat
N;Alternate names: neuromedin K receptor; NK-3 receptor
C;Species: Patrus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  337 VPSPESPASIPEKERPSSPSSGKGKTE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 372 GPV ATPSSIDLTSNOSSPSDSKTMTE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 LKGVWK------
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probable allatostatin receptor. 2 fruit fly (Drosophila melanogaster)
probables brosophila melanogaster
C.Species: Drosophila melanogaster
C.Bate. 08 Sep.2000 #sequence_revision by Sep.2011 #ter._phange 02-Aug 2002
C.Accession. JC731 #ter.
Blochem. Blophys. Res. Commun. 273, 571 577, 2000
A,Thie: Molecular cloning and genomic organization of a second probable allatostatin rev.
A,Reference number: JC7319
A,Rolecular type: MRNA
A,Residues: 1-357 < LBN>
A,Rolecular type: MRNA
A,Residues: 1-357 < LBN>
A,Cross-references: GB:AP25352
C,Comment: This receptor, belonging to the insect allatostatin neuropeptide family, which C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Superfamily: endothelin receptor B C;Superfamily: endothelin receptor B C;Keywords: extracellular protein; glycoprotein, neuropeptide; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 VMLLSIAIIEALLWLPEWVAWLWVWHLKAAGPAPPQGFIAL SOVLMFSISSANPL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 256 RLVVVVVIAEASIMIRPVQLILLA --LKSLDVIEINTLIKLVLQVIAQTLAVSSGCINFL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86 MEVILCIPHTATDYMVYYWPYGREWCRSVQYLİVVTAFASIYTLVLMSIDRFLAVVHPIR 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 -VAEBEMS--MEGKLIPLLAFGIPLFFASFYFWRAYDQTFFFFTFTULRUGIRS KQYT 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 FITWDFLGERTYQVPFFISSYLLELMISGLIMAMIMELMH 2010VFMJER13 GREEVT GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 SILLESAPIRATAYSKSUNDLGWFVÇKBSDWPIHTCMAAKSLTIVAYAKVOFMYASDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
10.1%; Score 218; DB 2; Length 357;
Best Local Similarity 25.1%; Pred. No. 6 8e-10;
Matches 78; Conservative 57; Mismatches 132; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: right arm of chromosome 3, 98D-E A,Introns: 180/3; 273/3; 326/3
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Job Lime : 23 secs
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OM protein - protein search, using sw model

Run on: January 28, 2003, 11:43:46; Search time 14 Seconds

03, 11:43:46 ; Search time 14 Seconds (Without alignments) 1202.8:4 Million cell updat⊬s/sec

le: US-09-828-412-1

Perfect score: 2167 Sequence: 1 MNVSFAHLHFAGGYLPSDSQ.

| uence: 1 MNVSFAHLHFAGGYLPSDSQ. . . ODNDPIPWEHEDQETGEGVK

Scoring table: BLOSUM62 Gapop 10 0, Gapext 0-5 Searched 112892 segs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 10% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

SUMMARIES	Description	ш	145 20855C	MOUSE P56479 mus mus	PAT 004726 rattu	M 043603 homo	P47211 homo	088626 raffi		HUMAN OF 0755 Row	MOUSE P30731	CAVPO P30547 cavis	F32745	mus ก	P14600 rat		-m-4 126614	097512 cryet	n 3Um 75979	P25103	FAT P16177 rattu		GP72_HTMAN Q9nym4 homo sapien	F35374		PAT P24053	Odako	BOVIN POSSACE		MOIJSE	HUMAN P50052 homo	MERUN Q92026 merio	084
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# ALIGNMENTS

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This SWISS-PROT entry is cupyright. It is predated through a collaboration between the Swiss institute of Public matters and the EMBL unit station. The the EMBL of this transfer as the second content is the second way non-profit institutions as long as its content is in to way maddified and this statement is not temoved. Usage by and for commercial entities requires a license agreement (See http://www.isb.sth.il/incline/or send an email to licensesish sib. ch.
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STAIN 129/5V

MEDILIBE 99048952, Fulked 9819122,

A Pang L., Hashemi T., Lee H.J., Maguire M., Graziano M.P., Bayne M.,

RA Hawes B., Wong G., Wang S.,

FT "The more Gal? Dilarin reseptor. Gen.min digiti.addisc. JONA

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FT Cloning, and functional characterization.";

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THE PHOSPHOLITASE C/PROTEIN KINASE C PATHWAY (VIA GQ. AND THAT

CO THE HIBIT ADENYLYL CYCLASE (VIA GI).

CO TENTIALIZATIVE EXCATION: Integral membrane protein.

SIMILARITY BELONS TO FAMILY I OF G-FECTERN SUPPLIES.
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MEDLINE=99048901, FubMed-982111,
MeDLINE=99048901, FubMed-982111,
MeDlakowski L.F JT. Noeill G.P. Howard A.P., Broussard S.R.,
Sullivan M.A., Feighner S.P., Sawddargo M., Nguyon T., Yardman S.,
Shiao L.-L., Hreniuk D.L., Tan C.P., Evans J., Abramovitz M.,
Shiao L.-L., Hreniuk D.L., Tan C.P., Evans J., Abramovitz M.,
Shao L.-L., Hreniuk D.L., Tan C.P., Gonney M.P., Tharian A.,
Khoshkonei A., George S.P., Smith P.G., O'Dowd B.F.,
"Molecular characterization and expression of closed human galumn
                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi.
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                              ORDS PROCESS (1972) (1872) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (1874) (18
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InterEro, IREC0074, GRCF_Phodpen
Pfam, PROCO17 7 Tm 1, 1.
PRINTS, PROCO17, GFORPHONOPEN.
PROSITE, PSOCO37, G_PROTEIN_RECEF_F1_1, 1.
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                                         STANDARD;
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GALS_MOUSE
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NCBI_TaxID=10116;
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Ollow 1997 (Rel. 35, Last sequence update)
Ollow 1997 (Rel. 40, Last annotation update)
Galanin receptor type 1 (Galler) (Galler)
Caller or Galler
Fathus reveging (Rel.)
Bathus revealers (Rel.)
Wetazoa Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                ) (POTENTIAL)
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PPOSITE, PSSG202, G PROTEIN RECEP F1.2, 1.
G-protein coupled receptor; Transmembrane, Glycoprotein;
Multigene family
                                                         EXTRACELLULAR (POTENTIAL).
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VF -> CL (IN PEF 2)
A -> V (IN REF. 2)
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                                                                                                                                                                                                                       -1. SUBCELLILAR LOCATION: Integral membrane protocol.
-1. TISSUB SPECIFICITY: SPINAL CORP. SMALL INTSCHINE, FINIAP
-1. TISSUB PROTECTION AND SEVERAL PERIND, PARTICLE, FINIAP
-1. HISPOLAMPUS, ANYZORLA, SUPRACITIC NOTICENO, HTW THALAMOS, THALAMOS,
-1. LATERAL PARARACHIAL NUCLEUS AND LOCUS COEPHIETS
-1. PTM THREE CYSTEINE RECIPIES ARE FOUND IN THE COURSELVE, ANY CALCUMATE,
-1. SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COURTIES FERRITY FOR
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                                                                                                    oning and characterization of the rat GALR1 galanin receptor tron
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                                                        Parker E.M., Izzarelli D.G., Nowak H.P., Mahle C.D., Bloom E.E., Wang J., Goldstein M.E.,
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F TENTIAL
                                                                                                                                                                 FUNCTION: RECEPTOR FOR THE HORMONE GALANIN, THE A TIVITY - RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITY APPROVADE
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PALMITATE (BY SIMILARITY)
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CYTCHLASMIC (POTENTIAL
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2 (POTENTIAL).
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Brain Res. Mol. Brain Pes. 24:179-189(1995).
-!- FUNCTION: RECEPTOR FOR THE HORMONE GALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to linonserich sibjob).
                                       MEDLINE=96363004; PubMed-8750821;
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                     TISSUE=Insulinoma;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: THREE CYSTEINE RESIDUES ARE FOUND IN THE C-TERMINUS, AT LEAST ONE OF WHICH MAY RE PAIMITOYLATED (BY SIMILARITY) SELONGS TO FAMILY 1 OF G-PROTEIN COUPLED PROEPTOPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomiës 45.438.508(1997).
-!- FUNCTION: RECEPTOR FOR THE HORMONE GALANIN. THE ACTIVITY OF THIS
-RECEPTOR IS MEDIATED BY G PROTEINS THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97415411; PubMed=9271210; Wang S., He C., Maguire M.T., Clemmons A.L., Burrier R.E., Guzzi M.F., Strader C.D., Parker E.M., Rayne M.L.; Rayne M.L.; "Genomic organization and functional characterization of the mouse
155 VGFIWALSIAMASPVAYYQRLFHRDSNQTFCWEHWP-----NQLHKKAYVVCTFVFGYL 208
                                          LPLFFASFYFWEAYDQCKKRGTKTQNLRNQIPSKQVTVMLLSIAIISALLWLPEWVAWLW 259
                                                                              200 LPLILIGECYARVLAHLHKK LPAMSKKSEASKKKTAQTVLVVVVFGISWLPHHVIHLW 267
                                                                                                                             260 VWHLKAAGPAPPQGFI ALSQVLMPSISSANPLIFLVMSEEFPFGLKGVWKWMITKKPP 317
                                                                                                                                                                 268 AEF--GAFPLTPASFFFRITAHCLAYSNSSVNPIIYAFLSENFRKAYKOVFKCRV---- 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=98635873, PubMcd-9367674;
Jacoby A.S., Webb 3.C., Liu M.L., Fofler E., Hort Y.J., Fathi Z.,
Bottema C.D.S., K., Shine J., Iismaa T.P.;
Bottema C.D.S., Shine J., Iismaa T.P.;
"Structural organization of the mouse and human GALRI galanin receptor genes (Galnr and GALNR) and chromosomal localization of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Choldata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                 P56479;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Galanin receptor type 1 (GALI-R) (GALRI).
GALP1 OP GALNET OP GALNE
                                                                                                                                                                                                                                                                                                                                                                  348 AA.
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Interpro; IPPAnnody74; GPCR Phodpsn
EMEM_ PF00001; 7tm 1, 1
PPINTS; PPP001?, GPCPPHONODSH.
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FEBS Lett. 411:225-230(1997).
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46 MGVLGNSLVITVLARSK-PGKPRSTTNLFILNLSIADLAYLLFCIFFGATVYALPTWVLG 104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36 VGFVGNLCVIGILLHNAWKGKP-SMIHSLILNLSLADLSLLLFSAPIRATAYSKSVWDLG 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 ---IMTVASILPLPEWFFSTIRHHEGVE-MCLVDVPAVAEEFMSMFGKLYPL--LAFG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200 LPLPPASFYFWPAYPOCYKPGTYTONLPNOIPSYCVTVMLLSIAIISALLWLPEWVAWI,W
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                                                                                                                                                                                                                                                                                      N-LINKED (GLCHAC...) (POTENTIAL.)
N LINKED (GLCHAC...) (FOTENTIAL.
N-LINKED (GLCHAC...) (FOTENTIAL.
BY SHILARITY
PALMITATE (BY SIMILARITY...)
GFS2D752BA19F9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         12.4%; Score 269; DB 1; Length 348; 28.3%; Pred, No. 6.8e-11; Live 54, Mismatches 178; Indels
                 Transmembrane, Glycoprotein;
                                              EXTPACELLINIAR (POTENTIAL)
                                                                                                                                                                           EXTRACELLULAP (POTENTIAL)
                                                                                                             EXTRACELLULAR (POTENTIAL)
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                                                                                                                             3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (FOTENTIAL)
N-LINKED (GLCNAC)
                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                             4 (POTENTIAL).
                                                                                              2 (POTENTIAL).
PPOSITE; PS50260; G_PPOTEIN_PECEP_F1_2; 1.
                                                               (POTENTIAL)
                                                                                                                                                                                            5 (POTENTIAL)
                                                                                                                                                                                                                             6 (POTENTIAL)
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                             Multigene family, Lipoprotéin, Palmitate.
DOMAIN
34 EXTPACPLIULA
                                                                                                                                                                                                            CYTOPLASMIC
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                 G-protein coupled receptor;
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                                                                              DOMAIN
TRANSMEM
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TPANSMEM
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.

Rattus norvegicus (Rat).

15-JUL-1998 (Rel. 36, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2022 (Rel. 41, Last annotation update) GALR2 OR GALNR2.

STANDARD,

GALS RAT

008726;

MEDLINE-97261892; PubMed-9108306; Howard A D , Tan C , Shiso L L , Palyha O C , McKee K.K., Weinberg D H , Feighner S D , Cascieri M.A., Smith R.G.,

TISSUE=Hypothalamus;

NCBI\_TaxID=10116; [1] SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning, pharmacological characterization and distribution of a nevel
                                                                                                                                                                                     Smith K F., Forray C., Walker M W., Jones K A., Tamm J A., Bard J., Branchek T.A., Linemeyer D.L., Gerald C., Expression cloning of a rat hypothalamic galanin receptor coupled to phosphoinsitide turnsver.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enanyi I.A.,

Brain Res. Mol Brain Res. 53.348-348(1998).

- PHRCTION FFERPITE FOR THE HERMANE BALANIN AND FOR GALP THE ACTIVITY OF THIS PECEPTOR IS MEDIATED BY G PROTEINS THAT ACTIVATE THE PHOSPHOLIPASE C/PROTEIN KINASE C PATHWAY (VIA GQ) AND THAT INHIRIT ADENYIAD CYCLASE (VIA GI).
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SIMILARITY: RELONSS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fathi Z., Cunningham A.M., Iben L.G., Battaglino P.B., Ward S.A.,
Nichol F.A., Pine F.A., Wang J., Goldsrein M.E., Iismaa T.P.,
                                                                                                                                                                                                                                                                                                                                                                       TISRIE-Hyporhalamus;
MEDLINE-9742833; PubMcd 9281594;
Mang S., Hashemi T., He C., Strader C., Bayne M.;
"Molecular cloining and pharmacological characterization of a new
galanin receptor subtype.";
Mcl. Pharmar-1 52 337 343(1927)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pathi Z., Cunningham A M., Then L.G., Rattaglino P B., Ward S A. Nichol K A., Pine K A., Wang C., Soldstein M.E., Ilsmaa T.P.,
Zimanyi I.A.;
                            "Molecular cloning and characterization of a new receptor for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pfam; PF00001; 7tm 1; 1. PrnNTS; PPANTATION PROBLES.
PROBLES, PPANTATO G PROPLEN PECEP F1 1; 1.
PROSTES, PSANTATO G PROPLEN PECEP F1 2; 1
G-profess coupled reoptor, TransmerExame, Slyciprotein, Milrigene family.
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EXTRACELLHUAR (POTENTIAL)
5 (POTENTIAL).
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van der Ploeg L H T , Sullivan F A ;
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InterPro, IPPA00276; GPCP_Phodpsn.
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                                                                               FEBS Lett. 405:285-290(1997).
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Borwasky B., Batacher T. A., Serial C. Orenial G.,
"Cloning and characterization of the human dalanin "Wilst receptor.";
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Bloomduist B.T., Beauchamp M.R., Zhelnin L., Brown S. E.,
Sore-Willse A.E., Steegor P., Cornfleld L.J.,
"Cloning and expression of the human glands regered to the L.
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Mammalia, Eutheria, Primates, Cafarihini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                  12.3%; Score 267; DR 1; Lobath 377;
25.1%; Pred. No. 9.96 11;
tive (0, Migratches 174; Indoles
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15-70L-1999 (Rel. 38, Last sequence update)
15-70U-2002 (Rel. 41, Last annotation update)
15-31D receptor type 2 (GALP2-P) (GALP2).
GALP2 OP GALNP2.
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SEQUENCE FPOM N.A. MEDLINE=9835135; FubMed-9685625; Fathi Z., Battaglins F.M., Then L.C., M. H., Baker B., Chang D.,

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This SWISS FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Richiformatics and the EMBL outstation the Burnpean Richiformatics Institute. There are not restrictions on the use by non-profit institutions as long as its content is in no way modified and this statement is not removed thangon by and for commercial entities require a license agreement (See http://www.ish.sih.ch/ann.unce/or send an email to license absence the second and email to license absence the second and email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to license and an email to lic
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SUBCELLULAR IOCATION: ILLEGRAI membrane protein.
TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY WITHIN THE CENTFAL
NERVOUS SYSTEM IN BOTH HYPOTHALAMUS AND HIPPOCAMPUS. IN PERIPHERA
TISSUES, THE STRONGEST EXPRESSION WAS OBSERVED IN HEART, KIDNEY,
                                                                                                                                                                                                                                                                             Kolakowski L F dr., o'Neill G P', Howard A D., Broussard S P., Sullivan K A., Peighner S.D., Sawrdargo M., Mguyen T., Kargman S., Shiao L. L., Heaniuk D.L., Tan C P., Evans J., Abramovitz M., Chareamenif A., Ordicher P. B., 19 G., Johnson M. P., Tharian A., Khashbouet H., Goorge P., Smith P.G., O'Dowd B P., "Molecular characterization and expression of cloned human galanin
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SIMILAPITY: RELONGS TO FAMILY 1 OF G-PPOTEIN COUPLED RECEPTORS.
McGovern P., Mahle F.D., Commun.
Dickinson P.R.F., Zimmaryi I.A.;
"Moleinson P.R.F., Zimmaryi I.A.;
"Moleinson Anaracterization, pharmacological properties and chromoseomal litalization of the human SALPE galanin receptor.",
Rrain Res. Mol. Brain Res. 58:156-169(1998).
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EMBL, AFG68696, AADG867111; -.
EMBL, AFG5762, AAC18118.1; -.
EMBL, AFG4782, AAC18618.1; -..
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-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- PTM: THPRE CYSTEINE RESIDUES ARE FOUND IN THE C-TERMINUS, AT LEAST ONE OF WHICH MAY BE PALMITOYLATED.
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Lorimer D D, Matkowskj K, Ronya P V;
"Cloning, chromosomal location, and transcriptional regulation of the
                                                                                                                  LSILLESARIBATATSESVWDLGWEVCKSSDWEIHTOMAARSLTITAVARVIENKASIFA 131
                                                                                                                                                                                                72 LOFILOCOPFOATIYILDGWVPGSLLCKAVHFLIFLTMHASSFTLAAVSLDRYLAIRYFL 141
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19 GGWHPB - AUTVPILLPALIFLVSTVSWTLVLAVILPGS QAUSTTH FILMISVAN 71
                                                                                                                                                                                                                                                                          GVENCLVPVFAVAEEFM
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homoi
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-/- PTROTION PESPITOR EQP THE HOPMONE GALANIN. THE ACTIVITY OF
PROBPTOR IS VEDIATED BY G PROTEINS THAT IMPLETS ADEMYLATE
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Mayaux J.-F.,
Mayaux J.-F.,
"Molecular cloning of a functional human jalanin resceptor.";
"Molecular Coad Soi "ISA 91:9780 9783(1994).
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Riochem Riophys Pes. Commun. 241:558-564(1997).
                                                                                                                                                                                                                                                                      132 KQVSIHKYTIMSVLVA---IMTVASLLFLPEMFFSTIRHHE
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01-FBB-1996 (Rel. 33, Last sequence update)
1K-0CT-20n1 (Fel 40, Last annotation update
Galanin receptor type 1 (GALI-R) (GALBI).
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4 (POTENTIAL).

EXTRACELLITARE (FOTENTIAL).
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EMBL, U53511; AAC51936.1; -.
EMBL, U90666; AAC95397.1; -.
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EMBL; U90659; AAC95397.1; JOINED.
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This SWISS-PROT entry is copyright. It is produced through the case sets is between the Swiss Institute of Bioinformatics, and the CTPB construction in the Burnopean Bioinformatics Institute. There are is restricted as a constitutions as the constitution and the constitutions as the constitution and the constitutions are reached. These by and the constitutions and increase the constitutions and the constitution and the constitution and the constitution and the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the constitution of the c
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Mammalia, Eutheria, Rodentia, Sciuroquathi, Muridue, Mornoes Barlos
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Cmith P. W. Marker W. Arrymychyn P., Hand J. B., wer'r B.,

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Pfam; PF6001; 7tm 1; 1.
PRINTS; PR00237; GF6RRHCD0FSN.
PROSTTE; PS60237; G PROTEIN REFER F1 1; 1.
PROSTTE; PS50262; G PROTEIN RECERF F1 2; 1.
G-protein coupled recepted; Transmombiano; Glycolocitis;
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Waters S.M., Krause J.E.;
Waters S.M., Conting requesting the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of the continuation of
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"VTOPLASMIC" (POTENTIAL)
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EMBL, AF031522, AAC26145.1; ...
EMPL, AF077799, AAC36943.1; ...
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Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 ALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEFREGLKG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  191 KLYPL----LAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRSKQVTVMLLSIAIIS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             193 YLLPVAVVSLAYGRTLCF----LWAAVGPA---GAAAAEAPRRATGRAGRAM-LAVAALY 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80 AAIYTLDAWLFGAFVCKTVHLLIYLTMYASSFTLAAVSLDRYLAVRHPLRSRALRTPRNA 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 WSVLVAIWTVASLLPLPEW FFSTIRHHEGVEMCL.....---VDVPAVAEEFMSMFG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             140 RAAVGLVWLLAALFSAPYLSYYGTVR-YGALELCVPAWEDARRRALDVATFAA-----G 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 ALCWGPHHALILGFWYGRFAFSPATYACRLASHCLAYANSCINPLVYSLASPHFRAPFRR 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 ATAYSKSVWDLGWFVCKSSDWFIHTCMAAKSLTIVVVAKVCFMYASDPAKQVSIHN-YTI 141
                                                                                                                                                                                                                                                                                                                           12.3%; Score 261; DB 1; Length 370;
24 f%; Pred No. 2 4e 10;
ative 53; Mismatches 155; Indels 60; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                             26 IFALLVAVCLVGFVGNLCVIGILLH...HAWKGKFSMIHSLILNLSLADLSLLLFSAFIR 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 VÉVIFALIFLIGMVGNGLVLAVLLQPGFSÁMQEPRSTTDLFÍLNLAVADLCFILCCVPFQ 79
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!- SUBCELLULAR LOCATION: Integral membrane protein.
!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vortebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=129/Sv, Kolakwaid A.D., Broussard S.R., Kolakwaid L.E., C.L., C'Neill G.P., Howard A.D., Broussard S.R., Sullivas F. A., Feighner S.D., Sawrdargo M., Nguyen T., Fargman S. Shiao L.-L., Hreniuk D.L., Tan C.P., Evans J., Abramovitz M., Chareanneuf A., Coulombe N., Ng G., Johnson M.P., Tharian A., Khoshbouei H., George S.P., Smith P.G., O'Dowd B.F., Tharian A., Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCGREPHPHHHPAHPALPPVQPASSGPÄGYPGDAPP 342
                                             CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
PALMITATE (BY SIMILARITY).
POLY-ALA.
                                                                                                                                                                    R -> S (IN REF. 3).
F -> Q (IN REF. 2).
R -> C (IN PEF. 2).
R -> C (IN PEF. 2).
W, CESB39E6147AFAD4 CRC64;
EXTRACELLULAR (POTENTIAL).
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15-JUL-1999 (Rel. 38, Last sequence update)
15-CCT-2001 (Rel. 40, Last annotation update)
Galanin receptor type 3 (GAL3-R) (GALR3).
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                       7 (POTENTIAL)
                                                                                                                                                                                                                                                                           40410 MW;
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                                                                                                                                                                                                                                                                        370 AA;
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088853;
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                                             DOMAIN
CARBOHYD
DISULFID
DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                           SEQUENCE
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DOMAIN
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entities requires a license agreement (See http://www isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 WSVLVAIWIVASLLPLPEW-FFSTIRHHEGVEMCL------VDVFNVAEDFNONFG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 RAAVGLVWLLAALFSAPYLSYYGTVR-YGALELCVPAWEDARRRALDVATFAA-----G :92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 KLIPL ---- LAFGLELFFASFTFWRAYEQCKFRGTKTGNLENGTECKCVTVMLLSIAIIS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247 ALLWLPEWVAWLWYWHLKAAGPAPPQGFIALSQVLMFSISSAMPLIFLVMSEEFPEGLKG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 ATAYSKSUWDIGWEVCESSDWFIHTGMAAFSLTIUUUVAFUCFWYAGFBAFQVSIBN TTI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26 IPALLVAVCLVSFVSNLCVIGILLH HAWKSKREMINSLILMLSLADISLLLFSAPIR 82
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                                                                                                                                                 Pfam; Provous,
PRINTS; PROCEST; GPCPPHONOBSN.
PROSITE; PSO0237; GPROTEIN RECEP F1 1; 1.
PROSITE; PS50262; GPROTEIN_PECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane, Glycoprotein;
Multigene family; Lipoprotein; Palmitate.

Multigene family; Lipoprotein; Palmitate.

EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR (POTENTIAL)
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7 (POTENTIAL)
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                                                                                                                                                                                                                                                                                                          1 (POTENTIAL)
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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24.4%; Pred. No 2 66-10;
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Galanin receptor type 1 (GAL3-P) (GALP1)
GALR1 OP GALNR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
                                                                                           MGD, MGI:1329003; Galr3.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
                                                                       EMBL; AF042783; AAC36588.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40390 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                              577
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308
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370 AA;
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Best Local Similarity
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Rest Local Similarity 24.7%; Pred. No. 36-10;
Matches 92; Conservative 55; Mismatches 164; Detrib 193
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Interpro; IPRGN0276; GPCR_Rhodpsn.
Pfan, PROMOD; 7tm 1; 1.
FRINCS, FELG. 1, 7fm 1; 1.
FRINCS, FELG. 1, 7fm 1; 1.
FROSITE; PSG0227; G PROTEIN RECEP P: 1; 1.
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Nature 402-489-495(1999).
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140 RAAVGINWILAALESAPYLSYYGTVR-YGALELGVPAWEDARRAALDVATFAA---- G 192
                              191 FLYPL----LAFGLPLFFASFYFWPAYDQCKKPGTRIQNIPNQIPSKQVTVMLLSIAIIS 244
                                                            CAAAAEAFFFATTFAGFAW . I.AVAATT 244
                                                                                        247 ALLWIPEWVAWIWVWHIKAAGPAPPQGFIALSQVIMFSISSANPLIFLVMSEEFFEGLKG 306
                                                                                                                     245 ALCWOPHRALILGEWYGFFAFSPATYAGPLASHCLAYANSCINPLYYALASPHFPAPPPP 304
                                                                                                                                                                                Propreherealphypeassapporpodarpsgrunagg 347
                                                                                                                                                                                                                                                                                                                             0.7531;
01-APR-1993 [Bel. 25, Created)
01-NOV-1995 [Bel 32, Last sequence update)
16-OCT-2001 [Rel. 40, Last annotation update)
Prohable G protein-coupled receptor GPR72 precursor (Glucocorticoid-
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INDUCTION - BY GLUCOCOPTICOIDS AND CAMP, IN T CELLS.
SIMILARITY. BELONGS TO FAMILY I OF 3-FEVEUR CHIPLED PRORPHOPS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Motazha, Chhrista, Craniata, Vertekrafa, Euteleosiomi.
Mammalia, Eutheria, Rodontia, Sciurognathi, Muridae, Murinae, Mus
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PRINTS, PRO0237, GPERHODOSN.

PPOSITE, PSG0287; G-PROTEIN RECEP F1 1, 1.

PPOSITE; PSG0282; G-PROTEIN RECEP F1 1, 1.

G-protein coupled receptor; Transmembrane, Glycoprotein; Signal, Alternative splicing.

SIGNAL.
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PPOBARLE G PPOTEIN-COUPLED RECEPTOR
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VPSSLCPALFTCKRPWPFQESQGALHOTLFPPLE ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 CSLHVSALTUTAIÄVDRHQVIMHPLKPRISITKGVIY--IAVIWYMATPFSLPHAICQKI. 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163 STIPHHEGY FMCLVPVPAVABEPMSMPSKLYFLLAFGLELFFASFYFWRAYDQ---CK COT
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                                                                                                                                                                                                                                                                                                                                   -> ORPWDFQESQSLHDTLFPPLE IN ISOFORM
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Bukaryota: Metarca, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Euthoria, Rodentia, Hystricognathi, Cavildae, Cavia.
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                                                                                                                                                            CYTOPIASMIC (POTENTIAL)
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MISSING (IN ISOFORM RP39)
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MEDLINE-92256498, FubMed=1374648;
Gorbulev V., Abbundova A., Duzius H., Fahrenholz F.;
3 (FOTENTIAL);
CYTOPLASMIC (POTENTIAL)
4 (FOTENTIAL);
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01-APR-1993 (Rel. 25, Last sequence update)
01-APR-1993 (Rel. 26, Last semotation update)
Substance P relyers (SFP) (UP-1 todeFill) (UP-1R)
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                                                                       (FCTENTIAL)
                                                                                                                                             7 (FOTENTIAL)
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Matches 101, Conservative
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[Latity 72.1%; Ried. Mc. 2.5c 38;
Conservative 80; Mismatches 159; Indels 64; Gaps
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Zhan M., Zhang G., Chissoe S., Murray J., Miller N., Minx P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Gyres M., Du.;, Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozersky P., Rohlfing T., Scheet P., Walker C., Wamsley A., Wohldmann P., Pepin K., Melson J., Korf I., Bedell J.A., Hiller L., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budarf M.L., McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Behamann L., Seroussi E., Fransson I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Than N., Milkinson P., Wright H.;
                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION Integral membrane protein.
TISSUE SPECIFICITY: BRAIN, PITUITARY AND PANCREAS.
SIMILARITY: BELUNGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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GLU-RICH (ACIDIC)
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                                                                                                                                                                                                                                                                                                                  "The DNA sequence of human chromosome 22.";
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EMBL; Z82188; CAB45263.1; -.
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HSSP; P34996; 1DDD.
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Ouery Match
10.6%; Score 229; DB 1; Length 418;
Best Local Similarity 23.4%; Pred. No. 3.4e-08;
Matches 83; Conscrvative 63; Mismatches 160; Indels 48; Gaps 11;
25 IIFALLVAVCLVGFVGNLCVIGILLHNAWKGKPSMIHSLILNLSLADLSLLIFSAPIRAT 84
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46 LIPLVYLVVCVVGLIGNSLVIYVVLRHT--ASPSVTNVYILNLALAD-ELFMLGLPFLAA 102

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This SWISS-PROT entry is copyright. It is produced through a cellaboration
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85 AYSKSUWDIGWFUCK---- SSPWPHHTOMAAMSLTTVUVARTOFNHASTFARGV 134
                                                                                                                                                                                                                                                                  252 PEWVAWLWYWHIKAAGPAPPO -- GFIALSQVLMFSISSAMFLIFIAWSERFREGLEGY 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pohl J.S., Peterson P.A.; "Molecular cloning of the murine substance K and substance P receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Immunol. 152:1830-1835(1994).
-!- FUNCTION: THIS IS A RECEPTOR FOR THE TACHYKININ NETROFERFILDE SUBSTANCE P. IT IS PROBABLY ASSOCIATED WITH G PROTEINS THAT ACTIVATE A PHOSPHATIDYLINGSITCL CALCIUM SECTNI MESSENGER SIGTEM.
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-!- MISCELLANEOUS: THE RANK ORDER OF AFFINITY OF THIS RECEPTOR TO TACHYKININS IS: SUBSTANCE P > SUBSTANCE K > NEUROMEDIN K.
-! SIMILARITY: BELONGS TO FAMILY 1 OF G PROTEIN COUPLEU KEUEPTORS.
                                                                                      135 SIHNYTIWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEEFMSMFGKLYF
                                                                                                                                 162 -----TVSAAVWVASAVVVLPVVVFSGV--PRGMSTCHMQWPEPAAAWRAGFTTYTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cook G.A., Elliett D., Metwali A., Blum A.M., Sandor M., Lynch R., Weinstock J.V.,
                                                                                                                                                                             195 LLAFGLPLFFASFYFWRAYDQCKKRGTKT---QNLPNQIPSKQVTVMLLSIALLSALLWL
                                                                                                                                                                                                                     212 ALGPEGELLVICLCYLLIVVKVPSAGPPVWAPSCQPPPRSEBRVTRMVVAVVALEVICWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                          103 QNALSYWPFGSLMCRLVMAVDGINQFTSIFCLTVMSVDRYLAVVHFTRSARWRIAFVAR
                                                                                                                                                                                                                                                                                                     272 Pryvini - - VIVVCPLPEEPAFFGLYFLVVALFTANSCANFLLIGFLSTRFKOGFR-
                                                                                                                                                                                                                                                                                                                                                       308 WKWMITKKPPTVSBSQETPAGNSBCLPPKVPSPESPASIPEKEKPSSPSSGKGK 361
                                                                                                                                                                                                                                                                                                                                                                                                   326 ----RVLLRPSPRVRŠQEPTVĞP----PEKTEREDE ---REERGRESPRGGKGK 363
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01-APR-1993 (Rel. 25, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Substance-P receptor (SPR) (NK-1 rereptor) (NY-1R).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 63-290 FROM N.A.
STRAIN=CBA; TISSUE=T-cell, and Brain;
MEDLINE=94165478; PubMed=8120392;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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22.6%; Pred. No. 4.5e 08;
tive 72; Mismatonos 165; Indels 64; Saps
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CYTORLASMIC (L.TENTIAL).
TALINNEE (SLINAI. ... (FOTENTIAL).
N LINNED (GLUNAC. ...) (FOTENTIAL).
BY SIMILARITY.
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BMBL, 127826; AAA17891.1; -.
PTR, $20394; S20304.
MGD, MGL198475; Tacri.
Interior, Imperior of GPCP_Phodpsn.
PFINE; PROCEST; GPCPPHOPPEN.
PFINE; PROCEST; GPCPPHOPPEN.
PROSITE; PROCEST; GPCPPHOPPEN.
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01-APP-1993 (Pel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Meuromedin P rooptor (PPP) (Neur-Kinin B receptor) (HF-4 1005Et)
NK-4R) (KIP) (Neurokinin 4 receptor) (NK4).
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKER (GLCNAC. .) (FOTENTIAL).

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PALMITATE (FOTENTIAL)

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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Proc. Natl. Acad. Sci. 11 S.A. 99-4124 4109(1902)
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                                                                                                                                                                                                                        10.5%; Score 227; DB 1; Length 407; 22 9%; Pred No 4 50.04; Live 71; Mismatches 165; Indels 6
            EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLITAR (POTENTIAL).
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MEDLINE-92237319, PubMed-1315051,
Xie G.-X., Miyajima A., Goldstein
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MEDLINE=97103087; Pubmed-8947459;
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Donaldson L.P., Haskell C.A., Hanley M.R.;
"Functional characterization by heterologous expression of a novel
cloned tachykinin peptide receptor.";
Biochem. J. 32011-5(1996).
PROCHEM. J. 32011-5(1996).
ROPPMEDIN THE IS A REPERTOR FOR THE TATHYTHIN MITS DEPTIDE
MEUPOWEDIN F (NEUFONTHIN B). THE FAHR CRIEF IF AFFIHITY OF THIS
PECEPTOR FO TATHYRININS IS: NEUFONTHIN K > SUBSTANCE K > SOKSIAN TE
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-trissub specificity: Highest levels in skeletal Moscle, Liver,
-trissub specificity: Low levels in Parkeras.
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HIGHEST TO OTHER TACHYKININS RECEPTORS.
-trissubscripts or other pachykinins (Fef 1) thought to be a kappa-type epost)
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Thertro, IPP601276, GPCP_Phedgen.
Thertro, IPP60137, Thm.1, 1.
PPINTS, PP00137, GPROTEIN RECEP_FI.1, 1.
PROSITE, PS00237, GPROTEIN RECEP_FI.2, 1.
PPOSITE, PSS0062, GPROTEIN PECEP_FI.2, 1.
G-grotein coupled receptor; Transmerent Stycoprotein, Lipopictein.
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Search completed January 28, 2003, 11-50:47 Job time : 16 secs

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Sequence 3, Sequence 2, Sequence 2,
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4: /cgn2_c/pto3ata/1/laa/6B_TOMB_pep.*

5: /cgn2_c/pto3ata/1/laa/pcTUS_TOMB_pep.*

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Maximum Match 100%
Listing first 45 summaries
                                      - protein search, using sw model
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Match Length DB
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72 USILLESAPIPATAYSKSUWPLGWFVCKSSDWFIHTCMAAKSLTIVVVAKVCPMYASDPA 131
                                                                                                                                              71 LCFILCCVPFQATIÝTLDDWVFGSLLCKAVHFLIFLTMHASSFTLAAVSLDRYLAIRYFM 130
                                                                                                                                                                                                                                                131 HSPFLR--TPRNALAAIGLIMGLALLESGPYLSYYSQSQLANLTVCHPAWSAPRPRAMPL 188
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                                                                                                                                                                                                                                                                                               189 ----FGKI YPLLAFGI PLEFASEYFWPAYDQGKKFGTKTQNLRNQIRSKQVTVMLLSIAI 244
                                                                                                                                                                                                                                                                                                                                               189 TEVESYLL PVI VISILTYARTI.HYI.MPTVPPV-AAGSGSGPAK----PRVTPMI VI VAV 242
                       10 GGYLPRERGOPWPTIIPALIVAVOLVGFVGNIGVILLHNAWKGKPSMIHSLILNLSLAD 71
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APPLICANT: Kolakowski, Lee F., Jr
TITLE OF INVENTION: MOUSE CALANIN PROEPTOR SALEZ AND
TITLE OF INVENTION: HUTLECTIPES FUNCOUS SAME
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COMPUTER: 18M Comparible
SOFTWARE: SYSTEM: Windows
SOFTWARE: Fast SEQ for Windows Version 2 ob
CHRPENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,424B
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P O Rox 2000, 124 E Lincoln Ave
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18-DEC-1997
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FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION.
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Patent No. 6337206
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TELECOMMUNICATION INFORMATION:
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LLNCIH: 371 amino acids
TYPE: amino acid
STPANDENNES: single
TOPOLOGY: line::
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PPIOP APPLICATION DATA.
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ZIP, 67045 6960
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CITY: Rahway
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US-08-993-424R-9
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CURRENT PILING DATE: 1998-11-25
WIMHER OF SEQ ID NOSE S9
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                                         12.5%, Shore 270.5, DR 4, Lenath Ph. 24.7%, Pred. No. 1.3e 14; active 61; Mismatches 178; Indets 41;
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APPLICANT: Smith, Kelli E.
APPLICANT: Branchek, Theresa A.
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Jones, Kenneth A.
                          Cuery Match
Best Local Similarity 24.7%
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; OPGANISM: Rat
US-09-199-737-5
US 09 993-424B-9
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                                                                                        200 LPILLICETYARVINHIHRY LYAMSRYCEASKRYTAQTVUNYTYTFSISWIPHHYJHIM 260
                                                                                                                                              260 VWHLPAAGBABGGBT - ALSQVLMFSTSSANPLIPLVMSBFFBFSTFFSTFFWKWLTKKFP ATT
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APPLICANT: FOLANOMENT, Lee F , Ur.
IIILE OF INVENTION: MOUSE GALARIN BECEFUSE GALRE AND
IIILE OF INVENTION: NUCLEOTIDES ENOCINS SAME
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12.4%, Scarc 269.5, DB 4,
Best Local Similarity 27.1%; Fred. No. 1.5e-14;
Matches RB; Conservative 60; Mismatches 120,
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SCETWARE TASISE for Windows Version 2.0b
APPLICATION DATA:
APPLICATION NUMBER: US/08/993,424B
FILLIG DATE: 18-DEC-1007
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O Box 2000, 124 E linech Ame
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 526 1777
CLASSIFICATION: 526 PRICE APPLICATION NUMBER: 60/033,851
FILING DATE: 27-DEC-1996
ATTORNEY/ASELT TRESPANTION
NAME HODE: Cheldan CA
                                                                                                                                                                                                                                    318 TVSESDETFACHSEGLEDKVPSPES 342
                                                                                                                                                                                                                                                                   221 - -- CNESPHGDAKE KANIDTIPS 340
                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3, Application US/08993424E; Patent No. 6337206; GENERAL INPORMATION:
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MEDIUM TYPE: Diskette
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MOLECULE TYPE: protein
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ZIP: 07065-0900
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US:08:993:424B-3
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                                                                                                                           268 AEF - GAPPLITPASPPPRITAHCLAYSNSVNPIIYAFLSENPPRAVRQVFFCPV---- 320
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           200 UPLEFASFYEWPAYDGTKKFGTYTGNURNGIESKGVTVMLLSIAIISALLWLFEWVAWIW 259
                                                209 LPLILLICHTYAKVINHIHKY-LYAMSKKSEASYKKTAQTVLVVVVPSISWLPHHVIHIM 267
                                                                                               260 VWHUKAAGPAPPQGFI--ALSQVIMFSISSANPLIFLVMSEEFPEGLKGVWHWMITKRPP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 WEVOKSSRWEIHTCMAAKSLTIVVVAKUCEMYASRRAKQVSI-HNYTIWSVLVA----- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              · TEFTUSMIVSIFILAAMSVIPTVAİVƏSPESSÉLFVSFMALLG 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *IMTVASLLPLPEMPFSTIRHHEGVE*MCLVDVPAVAEEFMGMFGKLYPL**LAPG*** 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.4%, Score 269.5, DB 4, Length 346,
27.1%; Pred. No. 1.5e-14;
tive for Mismarrhes 130; Indels 47; Saps
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Tan, Carina APPLICANT: Sullivan, Kathleen TITLE OF INVENTION: GALANIN PECEPTOP GALP2 AND TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME NUMBER OF SECTIONS 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEE: Merck & Co., Inc.
: P.O. Box 2000, 126 E Lincoln Ave
Rahway
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PRIOR APPLICATION DATA:
APPLICATION TIMBER: 60/033,851
FILING DATE: 27.DEC 1996
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
PEGISTFATION NIMPER: 38,179
                                                                                                                                                                                                                        321 -- CNESFAGDAKE EMRIDTEPS 340
                                                                                                                                                                                        318 TVSESQETPACHSECLPREVESPES 242
                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08993088A
Patent No. 6287855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594 1958
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IRM Compatible
SYSTEM: Windows
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Matches 88, Conservative
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COMPUTER: IF
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STATE:
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36 VSFVSKLOVIGILLENAMRGKE SMIRSLILKLELAGISLLLFSAFIRATARISEVWDLG 94
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Lenath 346;
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148 ---IWTVASLLPLPEWFFSTIRHHEGVE-MCLVDVPAVAEEFWSMFGKLYPL--LAFG-- 199
                                                                                         195 VORÍWALCIAMASPVAYYQRLEHPRONQTRÓWERNÉ - NOLHPPAYVVOTRVESYL 208
                                                                                                                                                                                                                                                                                                       209 LPLLLICFCYAKVLNHLHKK-LKNMSKKSEASKKKTAQTVLVVVVVFGISWLPHHVIHLW 267
                                                                                                                                                                                                                                                                                                                                                                                                     240 VWHERAAGPAPPGGFI--ALSQVIMFSISSANPLIFLVMSEEFREGLKGVWKWMITKKPP 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAFPLTPASFFFFITAHOLAYSVSVSPITYAFLSENFPPAYKQVPYCEV....320
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27.1%; Pred No. 1 co.14;
-ive - 60; Mismarches 130; Indels - 47; Sags
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OF THE SMITS OF THE SMITS OF THE SMITS OF THE SMITS OF THE SMITS OF THE SMITS OF THE SMITS OF THE SMITS OF THE SMITS OF THE SMITS OF THE SMITS OF THE 
                                                                                                                                                                                             200 IPLEFASEYEWPAYOG YYFFGIYTONLPROTPSYOVTVMILSIAIISALLWLPEWVAWLW
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APPLICANT: Berowsky, Beth
APPLICANT: Smith, Kellie
APPLICANT: Smith, Kellie
TITLE OF INVENTION: AND USES THERBOP
TITLE OF INVENTION: AND USES THERBOP
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CURRENT APPLICATION DATA
APPLICATION NUMBER: US/03/058,333A
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COMPUTER: IRM PC compatible
OPERATING SYSTEM: PC-DS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 TVSESOETPAGNSEGLPPKVPSPES 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       321 ----CNESPHGDAKE-KNRIDTPPS 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application US/09058333A Patent No. 6168812
GENERAL INFORMATION:
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REGISTRATION NIMBER - 28,678
PEPERBENCE/COFFI NIMBER - 527
TELEPHONE: 712 778 0400
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INPORMATION FOR SEG ID NO: 5:
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ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
TOPOLGGY: linear
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MOLECULE TYPE: DNA
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Best Local Similarity
Matches 99, Conserv
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US-09-058-333A-5
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MULHER REST TO JOHN 1. 19
                                                                                                                                                      200 IPLPPASPYPWPAYPQTKFMGTKTGNIPNOIPSKGVTVMHGGIATTGATTWTTGWVAWDW 719
                                                                                                                                                                                                                                                                                                                               260 VWHLKAAGPAPPOGFI -- ALSQVLMFSISSANYLIFLVMSEEFFFFILKSVWFWMITTKFFF 417
                                                                                                                                                                                                                                             209 UPLLIOPTARVIBHURFF (PRESERVIBETER) STORMANDER
148 ---IMTVASLLPLPEWFFSTIRHHEGVE-MCLVDVPAVAEHFMSMFSKLYTG LAFG
                                                                                                                                                                                                                                                                                                                                                                                  268 ABE - GAFPLIFAGFFFFITAHCLAYGUGUVAFTTYAFLOTUFFRAYEGUFFFV
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APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhin
IITLE OF INVENTION: G PROTEIN COUPLED PECEPTOR DETTEIN.
IITLE OF INVENTION: FROTUCION, AND USE THERRECE
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130 Water Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/04/513,974B
                                                                    155 VGETWALSIAMASEVAYTORLEHRU.NOTE.WEHWE
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PRIOR APPLICATION DATA:
APELIANTER HYMEER (FT/CFFF/01590
FILING DATE: 10 AUG-1995
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: 10 7 093989
FILING DATE: 15 AUG-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7 111NG DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APPLING DATE: APP
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PPIOP APPLICATION DATA:
APPLICATION NATA:
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FILING DATE: 28-DEC-1994
PRIOP APPLICATION DATA:
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30-SEF-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC-105/M3;
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N: 536
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PRICE AFFLICATION DATA:
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APPLICANT: Hosoya, Masaki
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PPICE APPLICATION DATA:
APPLICATION NUMBER:
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JP 6 189274

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NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179 REFERENCE/POCKET NUMBER: 196
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TELEPHONE, 732-594-1958
                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
                                                                                                                                                                                                                                                          TELEPHONE, 732-594-195
TELEFAX: 732-594-4720
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COMPUTER PEADARLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match
12.4%; Score 269; DB 3, Length 348;
Best Local Similarity 28.3%; Pred. No. 1.6e-14;
Matches 87; Conservative 54; Mismatches 128, Indels 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Tan, Carina
APPLICANT: Tan, Carina
APPLICANT: Sullivan, Kathleen
TITLE OF INVENTION GALANIN PECEFTOF GALFO AND
TITLE OF INVENTION. NUCLECTIBES ENCODING SAME
NUMBER OF SEQUENCES:
CORRESPONDENCE ANDPESS:
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STREET: P O Rox 2000, 126 E Lincoln Ave
FILING DATE: 11-AUG-1994
PPIOR APPLICATION DATA-
AFFLICATION UNMBER: JF 6 180273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
AFFLICATION NUMBER: JF 6-189272
FILING DATE: 11-AUG-1974
ATTOFNEY/AGENT INFOFMATION-
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US-08-993-088A-10
Sequent 10, Application HS/08493088A,
Parent No. 6287855
                                                                                                                                                                                               45753
                                                                                                                                                       NAME: Fesnick, David S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45'
TELECOMMINICATION INFORMATION:
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IRM Compatible
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INFORMATION FOR SEQ ID NO:
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MOLECULE TYPE: peptide
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MEDITM TYPE: DISKELL
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ZIF. 07065-0900
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Best Local Similarity 28.3%; Prod. No. 1.6e-14;
Matches 87; Conservative 54; Mismatches 128; Indels
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GENERAL INFORMATION:
AFELICANT: Tain, Carina
AFELICANT: Kolakowski Lee F., Jr.
TILLE OF INVENTION: MOUSE GALANIN RECEFTOR SALEL AND
TITLE OF INVENTION: NUCLECTIDES ENCODING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS: 120
SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/993,088A FILING DATE: 18-DEC-1997
CLASSIFICATION: 530
FRIOR APPLICATION: 570
FRIOR APPLICATION: TATA.
APPLICATION NUMBER: 60/033,851
FILING DATE: 27-DEC 1996
ATITORNEY/AGENT INFORMATION
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STPEET: P O POX 2000, 126 E Lincoln Ave.
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Patent No. 6337206
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COFFECTORECE ADDRESS:
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Best Local Similarity 28.3%; Pred. No. 1.60-14;
Matches 87; Conservative 54; Mismatches 109; Infals 19, Gaps
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130 WATER STREET
                   OPERATING SYSTEM: Windows
SOFTWARE: FastSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION WMBER: US/08/993,424B
FILING DATE: 18-DEC 1997
CLASSIFICATION: 536
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                                                                                                                                                                         AFFLICATION NUMBER: 60/033, 90.1 FILING DATE: 27 DEC 1996 ATTORNEY/AJENY INFORMATION. NAME: Heber, Sheldon O. REGISTRATION NUMBER: 39,179
                                                                                                                                                                                                                                                                                           REFERENCE/POCKET NUMBER, 191
TELECOMMUNICATION INFORMATION:
TELEPHONE: 732-594-1958
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APPLICANT: PURUGIMI, Shoji
APPLICANT: OHTAKI, TESSUYA
APPLICANT: HOSOYA, Masaki
IBM Compatible
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APPLICANT: ONDA, Haruo
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SEQUENCE CHARACTERISTICS:
LENGTH: 348 amino acids
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TELEFAX: 732-594-4720
                                                                                                                       CLASSIFICATION: 536
PRICE APPLICATION DATA:
APPLICATION NUMBER
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MOLECULE TYPE: protein
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  COMPUTER:
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                                                       269 AEF -GAFPLTPAGFFFFLTAHGLAYGHUGVHYLLYAFLGHHFFATF, UFF HYLLBHFF -GA
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28.3%; Pred. No. 1.66 14;
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                                                                                                                    | Sequence 44., Application 05/08513974B
| Patent No. 6114139
| GENERAL INPORMATION:
| APPLICANT HINDER Shuil
| APPLICANT HISTYA, Masaki
| APPLICANT: Pujii, Ryo
| APPLICANT: Ohtaki, Totouya
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REGISTRATION NUMBER: 34,235
REDECOMMUNICATION INPERMATION:
TELEPHONE: 617-523-340
INPORMATION FOR A440
INPORMATION FOR A521
SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
FILING DATE: 31 MAY-1995
APPLICATION NUMBER: 6 126610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER, IRM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 28-DEC-1994
APPLICATION NUMBER: 6-247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-0CT-1995
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                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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Best Local Similarity
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HS-08-513-974B-343
                                                                       COUNTRY, US
ZIF. 02109
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46 MGVLGNSLVITVLARSK PGKRRSTTNLFILMLSIARLAXLLKTRFGRATVTALTFWVIG 104
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                                                                                                                                                                                                                                                                                                         200 LELFFASFYFWRAYPGFRERGTFTGNLFNGIFSFQVIVWLLSIAI19A11M1FFRVAMIR 109
                                                                                                                                                                                                                                                                                                                                                    210 İBLILICECYARVINHIHKK-LKAMSYKSEACYKKTAQTVINTOTFSISKLPHHV7HLW 368
                                                                                                                                                                                                                                                                                                                                                                                           260 VWH!PAGDAPPJSPI--ALSOWIMFELSBANDLIFLVMSEEPPELLETTWEEFPELTETTFP 117 269 ABP--GAFDITPASFPPPITAHGLAYSNSSWNPITYAFISENPPAYPOVPKOHUTDSFP 126
                                                                                                                                                       105 APICK----FIH-----YPPTVSMLVSIPTLAAMSVDRYVAIVHSBRSSSIRVSRNALLS 15
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                            36 V3FVGNLCTISTLEHNAWKSKE SMIHSLIINESLATISGLIFSAFIBADAYDKSTWOLG 94
                                                                                                                                                                                                                148 ---IWTVASLLPLPEWFFSTIRHHEGVE-MCLVDVPAVAEEFMSMFGKLYFL--LAF3
                                                                                                                       95 WEVÇESSEWFIRTOMAAKSLIIVVVARVOEMYASDERAKOVSI-HNYIIRGVUVA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:

APPLICANT: Blocaquist, Brian T. , McCaleb, Michael L.,
APPLICANT: Cornfield, Linda J., Yoo-Warren, Heeja
TITLE OF INVENTION: Salamin Perepror and Nucleic Acid
TITLE OF INVENTION: Sequences
NUMBER OF SUCUENCES:
COPPESSONDENCE ADDRESS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S: Diskette, 3 % inch, 1 44 Mb storage
IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect for Windows version 6.1 CURRENT APPLICATION DATA:
APPLICATION NOMBER. US/08/665,034A
FILING DATE: 5 JUN-1996
AUTORNEY/AGENT INFERMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTRANDEDNESS: Single
; TOPOLOGY: Linear
; IMMEDIATE SOURCE:
; CLONE: Clone BMB77 amino acid sequence
US:08.665 034A.2
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REJSTRATION NYMBER 22888
PREPERENCY/COCKET NUMBER: WH SOL2-Orig.
TELECOMMUNICATION INFORMATION:
TELEPHONE. (202) 812 2705
INPORMATION FOR FEG. 10 NO. 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09665034A Patent No. 6410686
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West Haven
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MEDIUM TYPE: Diskette
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Best Local Similarity
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APPLICANT: Fukusumi, Shoji
APPLICANT obgi, Katuhitro
TITLE OF INVENTION: G PROTEIN COUPLED PEOPERN,
TITLE OF INVENTION: BRODUCTION, AND USE THEREOP
NUMBER OF SEQUENCES: 380
CORPRESPONDENCE ADDRESS:
                                                                                                                                        E: DIKE, RPONSTEIN, POBERTS & CUSHMAN, LLE
130 Water Street
                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NIMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
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PRIOR APPLICATION NUMBER: JP 6-236357
APPLICATION NUMBER: JP 6-33637
FILING NAME NUMBER: JP 6-33637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NAME:
PRIOR TOTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER. JF 6-189273
FILING DATE. 11-AUG-1945
FILING APPLICATION DATA.
APPLICATION NUMBER. JF 6-189272
FILING DATE. 11 AUG 1994
ATTORNEY/AGENT INFORMATION.
                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-POS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02 NOV 1994
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FILING DATE: 28-DEC-1994
FILING PAPLICATION DATA:
PRICATION NUMBER: JP 6-270117
FILING DATE: 02 NOV 1994
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30-SEP-1994
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 20-JAN-1995
PPIOP APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                      14-SEP-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 617-523-3400
617-523-6440
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NIMBER:
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                                                                                                                                                                                      Boston
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                                                                                                                                        ADDRESSEE:
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APPLICANT: Smith, Kelli E.
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Gerald, Christophe P.G.
APPLICANT: Branchek, Richard L.
APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
APPLICANT: Branchek, Theresa
TITLE CF INVENTION: BIA ENCODING A MAWMALIAN
TITLE CF INVENTION: BIA STEATIN PFEFFOR
TITLE CF INVENTION: AND USES THEREF
WINDER CF SEQUENCES: 14 USES THEREF
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COMPUTER: IRM PC Compatible
CERRAINS CHUIEM: FU-DUS/NS DUS
SCETWARE: Parent N. Fu-Dus/NS DUS
UNREWL APPLICATION DATA:
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1185 Avenue of the Americas
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Patent No. 5972624
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ATTORNEY/AGENT INFO-MATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFRENCE/CLETH HUMBER: 57233
TELECOMMUNICATION INFO-MATION:
TELEPHONE: 212,278,9490
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FORMATION FOR SEQ 1D NO. 8.
SEQUENCE CHARACTERISTICS:
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Spery March
Best Local Similarity 25.1%; Pred. No. 2.60-14;
Marches 93, Creservative Co. Wirmsteber 174;
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APPLICANT: Sollivan, Rathloon
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CONTITEE :PW Compatible
OFERATING SYSTEM. Willows
SOFTMON SYSTEM. Wildows Version 2.0b
CORENT AFFLICATION DATA:
APPLICATION NUMBER: US/08/993,088A
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                                     E: Merck & Co., Inc.
P.O. Box 2000, 126 E. Lindoln Ave
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/ Match 12.3%; Score 267; DB 4; Length 372;
Local Similarity 25.1%; Pred. No. 2.6e-14;
nes 93; Conservative 60; Mismatches 174; Indels 44; Gaps 11;
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APPLICANT: Tan, Carina
APPLICANT: Kolakowski, Lee F., Jr.

ITLE OF INVENTION: MOUSE GALANIN PECEFTOR GALR2 AND
TITLE OF INVENTION: NUCLEOTIDES ENCODING SAME
TITLE OF PROPERS: 18
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APPLICATION NUMBER: US/08/993,424B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Merck & Co., Inc.
P.C. Box 2000, 126 E. Lincoln Ave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JMBER: US/08/993,424B
18-DEC-1997
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REFERENCE/DOCKET NUMBER: 19846NP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08993424B
Patent No. 6337206
GENERAL INFORMATION:
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FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
LENGTH: 372 amino acids
TYPE: Amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                          MOLECULE TYPE: protein
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
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US-08-993 088A.2
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12.3%; Score 267; DB 4; Length 372;
25.1%; Pred. No. 2.6e-14;
tive 60; Mismatches 174; Indels 44; Gaps
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Job time : 19 secs
TELECOMMUNICATION INFORMATION:
                       TELEPHONE: 732-594-1958
TELEFAX: 732 594-4720
                                                                                                                                      . 372 amino acids
amino acid
                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acid
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                                                                                      INFORMATION FOR SEG ID NO:
                                                                                                                                                                                      single
                                                                                                                                                                                                                     MOLECULE TYPE: protein
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GenCore version 5.1 3 Copyright (m) 1993 - 1993 Copyright (m) 1993 - 1993
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OM profein - profein search, using sw model

January 28, 2003, 11 50 31 , Search time 13 Seronds Run on.

ODNOFIPWEHEDGETGEGVY 40A US-09-828-432-3 2167 Perfect score.

MINSFAHLHFAGGYLPSDSQ Sequence.

Gapop 10.0 , Gapext n 5 BLOSUM62 Scoring table:

Total number of hits satisfying chosen parameterer 122226 seqs, 20178551 residues Searched:

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Minimum DB seq length. A Maximum DB seq length. 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Watch 0%

Database :

Published Applications AA:\*

| cgn2\_6/prodata/2/pubpaa/USOB\_NEW\_PUB.pep:\*
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| cgn2\_6/prodata/2/pubpaa/USOF\_NEW\_PUB\_pep.\*
| cgn2\_6/prodata/2/pubpaa/USOF\_PUBCOMB\_pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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PRIOR FILING DATE: 2000-12-05
NUMBER OF SEO IN NOS: 10
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                                                                                                                                                                                                               , Sequence 3, Application US/039D9432
, Patent No. USD3CD31313DA1
, GENERAL INPORMATION:
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                                                                                                                       241 SIAIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSEEF 300
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APPLICANT: SHABON, HSMAN
TITLE OF INVENTION: MOLECULAR CLONING OF A GALANIN LIKE 7TM
TITLE OF INVENTION: RECEPTOR (AXOR40)
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PRIOR FLLING FAPE: 1999-08-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FARISE, for Windows Version 3 0
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CURPENT APPLICATION NUMBER 113/09/766,693
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PRICE APPLICATION NUMBER: US 09/417,170
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(Parent No. USD0010016337A)
(GENERAL INFORMATION:
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US-09-766-693-2
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APPLICANT: Berhold, Malin
TITLE CE INVENTION N. USECOLO137132A1c1 G Protein You jod Frequent
TITLE REFERENCE: 0045.US1
CURRENT APPLICATION NUMBER: US/09/628,432
CURRENT FILIND FATE: 2001.04.06
PRIOR APPLICATION NUMBER: G/210.u8
PRIOR PILING DATE: 2001.04.06
PRIOR APPLICATION NUMBER: G/251,313
PRIOR PILING DATE: 2000.04.06
NUMBER OF SEQ ID NOS: 10
SOFTWARE PERSONER OF SEQ ID NOS: 10
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APPLICANT: Glucksmann, Maria
APPLICANT: Glucksmann, Maria
APPLICANT: Glucksmann, Maria
TITLE OF INVENTION: METHOD CONTOUTIONS F HEWAN F
FILE REPERPORE: 38159 20044 00
CURRENT APPLICATION NUMBER: US/10/080,960
PHOR APPLICATION NUMBER: US/242,040
                                                     Sequence 2, Application UG/00828432; Patent No. US20020137132A1; GENERA INFORMATION; APPLICANT: Vogeli, Gabriel; APPLICANT: Lind, Peter
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; Publication No. US20520197695A1
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ONDA, HARUO
TITLE OP INVENTION, GALANIN RECEPTOF PROTEIN,
NUMBER OF SEQUENCES: 17
TYPE: Amino acid
TOPCLOSY: Linear
MOLECULE TYPE: Peptide
SECUENCE DESCRIPTION: SEQ ID NO: 2:
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TELETHINE: 617 523-3400
TELEFAX: 617-523-6440
INPURMATION FIRE SEY ID NO. 2:
SEQUENCE CHARACTERISTICS:
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// Publication No. US20030008329A1
// GENERAL INFORMATION:
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FUKUSUMI, Shoji
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HOSOYA, Masaki
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ONDA, HATUO
TITLE OF INVESTITA SALAHIM PETEPPOP (POCECH, (POCUTITA AME USE THEPETP
NUMBER OF SEQUENCES: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 VAEBFMSMFGKLYPLLAFGLPLFFASFYFWRAYDQ~KKRTQNLPNQIPSKQVTVMLL. 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HSLILMLSLADLSLLLFSAPIPATAYSKSVWDIGWFVYPSSDWFIHTMAAFSLTIVVVA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  o; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94 8%, Serre 2015, 28 %, Length 461, 100 0%; Pred. No. 8.74-167; Live. 0, Mismatches 0; Indels
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PRIOR FILING PATE: 2000 10-20
PRIOR APPLICATION WIMERP. 10 G0/242,039
PRIOR FILING DATE 2000-10-20
PRIOR FILING DATE: 2000 10-20
PRIOR FILING DATE: 2000 10-20
PRIOR FILING DATE: 2000 10-20
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PRIOR FILING DATE: 2000 10-20
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SEQ TONOS: 37
SEQ ID NOS: 37
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COMPUTER: IRM Compatible
OPERATING SYSTEM: POS
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STREET: 130 WATER STREET
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Publication No. US20030008329A1
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OHTAKI, Tetsuya
HOSOYA, Masaki
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COMPUTER PEADABLE FORM:
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US-10-080-960-5
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Fiblication No. US20020194457A1
GEMERAL INFORMATION:
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Best Local Similarity 24.5%;
Matches 101; Conservative
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OPGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 ---IWTVASLLPLPEWFFSTIRHHEGV------EMCLVDVPAVAEEFMSMFGKLYPL- 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 TEVESTILIBILITATORYARVINELHER-LENMSFESEASFFFTAGTVLVVVVEGTSWIF 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156 VGCTWALSTAMASP-----VAYHQALFHPPASNQTFCWEQWPDPPHF-----KAYVV1 (4)
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      ADDRESSER & CISHMAN STREET, FORESTS & CUSHMAN STREET: 130 WATER STREET CITY, BOSTON
                                                                                                                                                                                                                                     SOFTWARE Past SEQ Version 1 5
CURPENT APPLICATION DATA:
APPLICATION NUMBER: US/10/090,569
FILING DATE: 04-Mar-2002
CLASSIFICATION: <unimage-
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/540,650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11: MITEMPPTUSESQETPAGNSEGLPDFVPSPES 342
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TELECOMMUNICATION INFORMATION.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 31-MAY-1995
APPLICATION NUMBER: 6-326610
FILING PATE: 28-PE-1994
APPLICATION NUMBER: 6-247599
FILING PATE: 13-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-OCT-1995
APPLICATION NUMBER 7-134412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 34,235
                                                                                                                                                                       MEDIUM TYPE, Diskette
COMPUTER: IRM Comparible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617-522-3400
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                                                                                                                                                       COMPITTED PEADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: Amino acid
TOPOLANY: Linear
MOLECULE TYPE: Peptide
CORPESPONDENCE ADDRESS
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                                                                                    STATE:
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; Sequence 2, Application MS/A99A3396A

US-09-903-396A-2

RESULT 7

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APPLICANT: Allen, Keith D.
TITLE OF INVENTION. TRANSCENIC MICE CONTAINING
TITLE OF INVENTION. GLUCCCORTICOLD INMITED BETTER: FEWER TITLE OF INVENTION GLUCCCORTICOLD INMITED BETTER: FOR THE FERRENCE: P-359
CURRENT APPLICATION NUMBER: 10 6/217,179
PRIOR APPLICATION NUMBER: US 6/217,179
PRIOR APPLICATION NUMBER: US 6/217,179
PRIOR APPLICATION NUMBER: US 6/212,299
PRIOR FILING FATE: 2000-01-16
PRIOR APPLICATION NUMBER: US 6/22,299
PRIOR APPLICATION NUMBER: US 6/22,205
PRIOR APPLICATION NUMBER: US 60/22,205
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24.5%; Pred. No. 1.5e 12;
"Ye - 60; Mismatchos 124; Tedote "T; Supr
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SOPTWARE: FastSEQ for Windows Version 4.0
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*MEGKLYPILAFGLPLFFASFYFWRAY ** DQCKKFGTKTQNURNCIPS 131
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PRIOR APPLICATION NUMBER: Japan 8-021562
AFFICATION NUMBER: Japan 8-021562
FILING DATE: 2-JUL-1996
ATTOENEY/ASENT INFOFMATION:
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CURRENT AFRICATION DATA:
ARRICGATION NUMBER US/08/796,570A
FILING DATE: 06.FEB-1997
                                                                                                      233 KQVTVMLLSIAIIS-ALLWLPEWV-----
                                                                                                                                                                                                                                                                                                                                                                             | Sequence 1, AFEL 31 in UN. 1973/STDA
| Patent No. USB002009771A1
| GENERAL INFORMATION:
| GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 47147
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PEGISTRATION NUMBER: 30,628
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TELEPHONE: 617-523-3400
TELEFAX. 617-523-6440
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MOLECULE TYPE: Peptide
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       192 AEEFMS-
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US-08-796-570A-1
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APPLICANT: Annis, David Allen
APPLICANT: Raghatgi, Krishna
APPLICANT: Rash, Huw M
TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
FILE REFERENCE: 111025, 173, 173
                                                                                                                           10.3%; Score 224; DB 9; Length 488;
23.6%; Fred. No. 2 14-11;
tive 62; Mismatches 133; Indels 58; Gaps
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10 3%; Score 224; PR 9; Length 505;
Best Lonal Similarity 23.6%; Pred. No 2 20 11;
Matches 79; Consorvativo 62; Mismatches 133; Indels 58; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 RYMAIIDPLKPPLSATATKI--VIGSIWILAFLLAFPOONYSKTKUMPGRTLÖFVONPEG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                192 AEEPMS----- MPGKLYPLLAFGLPLFFASFYFWPAY- - D@CYPPGTYTGNI,FNQTFS-232
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                                                                                                                                                                                                                                                                                                                             63 LILMLSLADLSLLIFSAPIPATAYSFSVWPLGWFVCKSSDWFIHTCMAAKSLTIVVVAKV 122
                                                                                                                                                                                                                          16 PSDSQDWRTII-----PALLVA------VCLVGFVGNUCVIGILLHNAWKGKPSMIHS 62
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"IREPLY FILING PATE: 2077 03 28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR PATE: 2070-17-29
NUMBER OF SEQ ID NOS-34
SOFTWARE: FASESEQ for Windows Version 4.0
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; Patent No. US20020164617A1
                                                                                                      Ouery Match
Best Lical Similarity 23.6%,
The Amer 78, Conservative
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                          TYPE: FRT
ORGANISM. Human
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                                                               US-10-029-009-9
LENGTH - 4 PR
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Post Local Similarity 20.2%, Pred. No. 9.26-11;
Matches 95, Conservative 65, Mismatches 159, Indebs 109, Tays
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257 PKQHFTYHIIVIILVYCFPLLIMGITYTIVGITLWGGEIPGGTGDR -
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APPLICANT REPARCHED THE APPLICANT CHARD CHARD R
TITLE OF INVENTION WOLFFE DESCRIPTION OF THE CHARD R
TITLE TELEMING DATE: 1994-11-25
FRICE APPLICATION NUMBER: 69/20, 67
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Post Local Similarity 24.1%; Pred. No. 1.76 1.3
Matches 82; Conservative 57; Mismatches 156, 11.6 or 45;
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PRIOR APPLICATION DAIA:
APPLICATION NOBER: 08/796,570
FILING DAIE: 06-EEB-1997
AFFLICATION NUMBER: Capai 9-021562
FILING DAIE: 2-UUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Elsenstein, Ronald I.
REGISTRATION NUMBER: 30,628
REREFENSING/CORET NUMBER: 47147
TELEPHONE: 617-523-3401
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US-10-067-477-1
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                                                             184 FF-----MSMFGKLYPLLAFGLPLFFASFYFWRAYDQCKKRGTKTQNLRNQIRS---KQV 235
                                                                                                                    204 SWPLAHHPTIYTTFLII.FQYCL.PLGFILVCYAPIYPPLQRQGPVFHKGTYSL.PAGHMFQV 263
                                                                                                                                                                               236 TVMLLSIAIISALLWLPEWV AWLWVWHLKAAGPAPPOGPIALSCVLMFSISSANFLIFL 294
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145 NPTGWPPSISQAYLGIVLIWVIACVLSLPFLANSILENVFHRAMSKALEF-LADKVVCTE 103
                                                                                                                                                                                                                                         264 NVVLVVMVVAFAVLWLFLHVFNSLEDWHHBAIFICHGNLIFLVCHLLAMASTCVNFFIYG 323
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Patent No. US2G02111473A1
Patent No. US2G02111473A1
APPLICANT: ZASTAWNY, Roman L.
APPLICANT: MCWHINNIE, Elizabeth A.
APPLICANT: NC TILLE OF INVENTION: No. US2G020111473A1el G Protein Coupled Receptor FILE REPERENCE: 9074-9001
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                                                                                                                                                                                                                                                                                                295 UMSEEPPPGLKGUWFWMITFFFPPFUSESQETPACHSEGLP 334
                                                                                                                                                                                                                                                                                                                                                       324 FLNTNFKKEIKAL------VLTCQQSAPLEESEHLP 353
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EARLIER APPLICATION NUMBER: 18 60/081,995
EARLIER FILING DATE: 1999-4-16
SOFTWARE: PATENTIN VOS: 20
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CUPPENT FILING DATE: 1999-04-16
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US-09-292-973-2
'Soquence 2, Application US/09292973
'Patent No US20020111473A1
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US-09-292-973-19
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US-09-292:973-19
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Bost Local Similarity 24.5%; Pred. No. 6.7e-10;
Matches 91; Conservative 54; Mismatches 170; Indels 57; Japo
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APPLICANT: ZASTANNY, Roman L.
APPLICANT: ZASTANNY, Roman L.
APPLICANT: MCWHINNIE, Elizabeth A.
TITLE OF INVESTION No. 182002011147781-1 G Fritein Coupled Reseptor
THE PEPEPROG: 9044-9094
CUPPENT APPLICATION NUMBER: US/09/202,973
CUPPENT FILING PATE: 1999-04-16
EAPLIER FILING PATE: 1998-04-16
NUMBER OF SEG ID NOS: 20
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                                                                                                                                               APPLICANT: Allen, Keith D.
TILLE OF INVENTION. ELITA OFFICES AND METHODS RELATING THERETOFILE OF INVENTION. CONFOSITIONS AND METHODS RELATING THERETOFILE PERFERICE: R-678 CONFOSITIONS AND METHODS RELATING THERETOCUPPENDE PROFICATION NUMBER: US/10/112, 599A
CUMPENT FILLING DATE: 2002-09-05
PPTOP APPLICATION NUMBER US 60/280,513
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Best Local Similarity 23.8%; Pred. No. 8.1e-10;
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NUMBER OF SEQ ID NOS: 6
SOFTWARE: PastSFQ for Windows Version 4.0
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ORGANISM: Mus musculus
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US-10-112-599A-2
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                                                                                                          SEQ ID NO 2
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Search completed: January 28, 2003, 11:52:41 Job time : 15 secs